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GenCore version 5.1.6
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model 3.8 - protein search, using OM protein ; Search time 133.689 Seconds (without alignments) 659.602 Million cell updates/sec October 26, 2005, 15:28:42; Run on:

US-09-545-998B-2 1301 Title: Perfect score:

1 MGAWAMLYGVSMLCVLDLGQ.....PEEERGEQTEEKCHLGGRWP 228 Sequence:

2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description			Ada09440 Murine GI	Adh43110 Mouse glu	Mouse	_	_	Amino	Human	Human	Aay71467 Human PRO	Aab27651 Human pro	Human	Human	Human	Aab20115 Human imm	_	Aab47289 PRO364 po	Aab50982 Human PRO	Aab50910 Human PRO	Aae28161 Human TR1	Abu08442 Amino aci	Aao16574 Human tum	Aao23091 Human ene	Adn39966 Cancer/an
ATT. 100	ΩI	AAW37838	AAW49016	ADA09440	ADH43110	AAW49018	AAW49017	ADR46662	AAW37839	AAY06605	AAB33431	AAY71467	AAB27651	AAY95895	AAB24409	AAB47054	AAB20115	AAB53090	AAB47289	AAB50982	AAB50910	AAE28161	ABU08442	AA016574	AA023091	ADN39966
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	Score	1301	1301	1301	1301	1079	1079	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5
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Adh43131 Human TNF Adl91869 Human PRO	Human	Human	Trunca	Human	Human Tumour	Aae28158 Human TR1 Abu08439 Amino aci	Aao16575 Human tum Ada09435 Human TR1	Aao23092 Human ene Adh43105 Human INF	Human
ADH43131 ADL91869	ADOZ 0289 ADP55559 ADT94287	AAY44825 AAO16576	AA023093 AAW37840	AAO16577 AAO23099	AAY95879 AAY52158	AAE28158 ABU08439	AAO16575 ADA09435	AAO23092	ADO20305
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26	7 7 8 7 8 8	32	33 4	32	37	39	4 4 5	14.	4 4

ALIGNMENTS

Mouse 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoietic cells; lymphoid cell; autoimmune disorders. Amino acid sequence of the mouse 312C2 T cell protein. AAW37838 standard; protein; 228 AA. (first entry) 28-JUL-1998 AAW37838; RESULT 1 AAW37838

Mus sp.

WO9806842-A1 19-FEB-1998.

96US-00689943. 97WO-US013931 14-AUG-1997; 16-AUG-1996; 07-OCT-1996;

(SCHE) SCHERING CORP.

Gorman DM, Randall TD,

Zlotnik A;

WPI; 1998-159534/14. N-PSDB; AAV19152. treating, e.g. and other T Isolated 312C2 T cell gene - used to develop products for cancers, auto-immune disorders, transplantation rejection cell disorders.

Claim 2; Page 57-58; 71pp; English.

This is the amino acid sequence of the mouse 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells,

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Riccardi C;
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e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders
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                                                                                                                                                              121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLIVIFLVMAACIFFLTTVQLGLHIWQL 180
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                                                                                                                                                                                                                                                                                                                    Mouse glucocorticoid induced TNFR-family related protein; lymphocyte, GITR; tumour necrosis factor; apoptosis; hodgkin's disease; GITR-B;
                                                                 Gape
                                                                                                                                                                                                                                                                                                   Mouse glucocorticoid induced TNFR-family related protein (GITR).
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                                                                0; Indels
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                                              100.0%; Score 1301; DB 2;
100.0%; Pred. No. 1.6e-112;
iive 0; Mismatches 0;
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/note= "Cysteine pseudorepeat"
/note= "Cysteine pseudorepeat"
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'note= "Cysteine pseudorepeat"
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/note= "Signal peptide"
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154. .176
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                                                                Matches 228; Conservative
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                              Sequence 228 AA;
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GITR-C.
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                                                                                                             New isolated glucocorticoid induced TNFR related polypeptide - used to stimulate lymphocyte activity and cell death rescue, useful to, e.g. develop products to suppress lymphocyte activity and induce apoptosis.
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100.0%; Score 1301; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.6e-112;
Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                             Claim 13; Page 36-37; 53pp; English
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WPI; 1998-333315/29.
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                                          N-PSDB; AAV32773
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98US-00176200.

97US-0063212P

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(HUMA-) HUMAN GENOME SCI INC.
                              WPI; 2003-352290/33.
                                                                                                                              Sequence 228 AA;
                          Ni J, Ruben SM;
                  21-OCT-1997;
 Mus musculus
     US6509173-B1
             21-OCT-1998;
         21-JAN-2003
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The present invention relates to the isolation or noves number to concerosis factor (TNF) receptor-like proteins, designated TR11, TR115V1 and TR115V2 receptors, and the polymucleotide sequences for TR11, TR115V1, and TR115V2 receptors, and the polymucleotide sequences for TR11, TR115V1, and TR115V2 are useful in assays to test one or more biological activities of TR11, TR115V1 and TR115V2 polypeptides, for proliferation, as markers or differentiation and mobilisation of immune cells, and as markers or detectors of a particular immune system disease or disorder. They are also useful in treating or detecting deficiencies or disorder. They are calco useful in treating or detecting deficiencies or disorders of the amatopoletic cells, to increase differentiation and proliferation of hematopoletic cells, to increase differentiation and proliferation of detectors calcourse associated with a decrease in haematopoletic cells. Including pluripotent stem cells in an effort to treat disorders are also useful for modulating haemostatic or thrombotytic calcuty, for treating blood coagulation disorders, blood platelet disorders or wounds resulting from trauma, as well as for treating stroke, myocardial infarction and scarring. They may be used for detecting or treating autoimmune disorders (e.g. Addison's disease, clabetes mellitus, multiple crown as asthma, for treating and/or preventing organ rejection or graft versus host disease (dishetes mellitus, multiple cortical manufactions and cancers, for treating or modulating inflammation (e.g. septic shock and sepsis, isothermia-reperfusion injury, endotoxin celebality, induced lung injury and crohn's disease), beterting or treating or electing infections agents in electing or detecting infections agents in sources are also useful in expronse against infectious chemetriating, proliferating and attracting cells for tissue the polymucleotide sequences are also useful in exproprient and electing inferentiating and injury and differentiating and entering and electing inferentiation
Novel nucleic acids encoding human tumor necrosis factor receptor-like proteins TR11, TR11SV1 and TR11SV2, useful for treating blood coagulation disorders, blood platelet disorders, stroke and myocardial infarction.
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                                                                                                                                                                                                                                                                                                                                                                                present invention relates to the isolation of novel human tumour
                                                                                                                                                                                                                                                                       Disclosure; Fig 4; 70pp; English.
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The invention describes an isolated antibody (I) or its portion specifically binding to a protein chosen from a protein with amino acid residues 1-62 or 51-62 of a fully defined TRIISV1 receptor sequence of 241 amino acids (S1) as given in specification, and a protein with amino acid residues 38-49 of a fully defined TRIISV2 receptor sequence of 240 Novel isolated antibody binding to TR11SV1/TR11SV2 receptor, useful for treating inflammation, Paget's disease, thyroiditis. Disclosure; SEQ ID NO 7; 135pp; English. 30-OCT-2002; 2002US-00283105 98US-00176200. 99US-0121648P. 99US-0134172P. 2000US-00512363. 2000US-0221577P. 2001US-00915593. 30-OCT-2001; 2001US-0330757P. (HUMA-) HUMAN GENOME SCI INC. WPI; 2004-068938/07. Ruben SM; 23-FEB-2000; 28-JUL-2000; 27-JUL-2001; 13-MAY-1999; 24-JUL-2003. 21-OCT-1997; 21-0CT-1998 24-FEB-1999; 16-JUL-1999; ö 09 9 1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 1 MGAWAMLYGVSMLCVLDLGQPSVVBEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 0; Gaps 100.0%; Score 1301; DB 6; Length 228; 100.0%; Pred. No. 1.6e-112; 0; Indels 0; Mismatches Query Match Best Local Similarity 100. Matches 228; Conservative

120

61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT

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immunostimulant; antirheumatic; dematological; antirhyroid; haemostatic;

mutiasthmatic; antirheumatic; devostatic; proliferation inhibitor;

mitiasthmatic; antiarthritic; cytostatic; proliferation inhibitor;

differentiation inhibitor; T-cell chemotaxis inhibitor;

mitiation inhibitor; T-cell chemotaxis inhibitor;

RAILSV1; TRILSV2; tumour necrosis factor receptor-like protein;

TRILSV1; TRILSV2; tumour necrosis factor receptor-like protein;

TNF receptor-like protein; inflammation; bone disease; Paget's disease;

MIDIOPERIORIS craniomecaphyseal dysplasis;

MIDIOPERIORIS craniomene progressiva; gigantism; osteoclastoma;

MIDIOPERIORIS; autoimmune thyroiditis; immunodeficiency disorder;

MIDIOPERIORIS; autoimmune thyroiditis; immunodeficiency disorder; thrombocytopenia; TRII;

MIDIOPERIORIS; Albatelet disorder; thrombocytopenia; TRII;

MIDIOPERIORIS ALPARITICAL ALPA 61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120 121 NCSOPGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL Mouse glucocorticoid-induced tumour necrosis factor receptor (GITR) antiinflammatory; osteopathic; immunosuppressive; neuroprotective; RROHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP 228 tumour nerosis factor receptor family; mouse; glucocorticoid-induced tumour necrosis factor receptor; GITR Ä ADH43110 standard; protein; 228 (first entry) US2003138426-A1. Mus musculus. 25-MAR-2004 ADH43110; 181 RESULT 4 ADH43110 셤 셤 ò 8

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amino acids as given in specification. (I) is useful for detecting tumour necrosis factor (TMF) receptor-like proteins TR11SV1 or TR11SV2 protein to a biological sample, which involves contacting the biological sample with (I), and detecting the TR11SV1 or TR11SV2 protein in the biological sample. (I) is a labeled antibody, the label is chosen from an enzyme label, a radioisotope, a fluorescent label, and biotin. The method described is useful for treating inflammation. Also described is method useful for treating bone disease or a disorder such as Paget's disease, of the operrosis, craniometaphyseal dysplasia, fibrodysplasia ossificans progressiva, gigantism, or osteoclastomm. (I) is useful for treating autoimmune disorders e.g. autoimmune haemolytic anaemia, autoimmune disorders e.g. autoimmune haemolytic anaemia, autoimmune disorders e.g. severe combined immunodeficiency and Wiskott-Aldrich syndrome. (I) is also useful for treating rheumatoid arthritis, systemic lupus erythematosus, graft-versus-host disease, casthma, cancer, Grave's disease, blood coagulation disorders and platelet disorders (thrombocytopenia). This is the amino acid sequence of mouse gluocoorticoid-induced tumour necrosis factor receptor family members
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1301; DB 8; Length 228; 100.0%; Pred. No. 1.6e-112; ive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW49018 standard; protein; 222 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA & UPJOHN SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96GB-00025074.
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                                                                                                                                                                                                                                                                                                                                                                                    TR11, TR11SV1 and TR11SV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse glucocorticoid
GITR; tumour necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-333315/29.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 228 AA;
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The present claimed sequence represents a mouse glucocorticoid induced TNRF-family related protein variant C (GTR-C). The invention also claims for GTR (AAM49016) and GTR-B (AAM49017) The GTRs are claimed to be useful for stimulating lymphocyte activity and cell death rescue. GTR antagonists are claimed to be useful for suppressing the lymphocyte activity and for inducing apoptotic deletion. GTR cDNAs and the proteins they encode are also claimed to be useful for suppressing growth of tumour cells over-expressing GTR or for the treatment of refractory
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                          New isolated glucocorticoid induced TNFR related polypeptide - used to stimulate lymphocyte activity and cell death rescue, useful to, e.g. develop products to suppress lymphocyte activity and induce apoptosis.
                                                                                                                                                                                                                                                                                                                                                                               1 MGAWAMLYGVSWLCVLDLGQPSVVEEPGCGFGKVQNGSGNNTRCCSLYAPGKEDCPKERC
                                                                                                                                                                                                                                                                                                                                                                                                                        61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT
                                                                                                                                                                                                                                                                                                                                                              1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC
                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse glucocorticoid induced TNFR-family related protein; lymphocyte;
GITR; tumour necrosis factor; apoptosis; hodgkin's disease; GITR-B;
GITR-C.
                                                                                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                                                                                    Length 222;
                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                  82.9%; Score 1079; DB 2;
100.0%; Pred. No. 6.4e-92;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                       Claim 15; Page 43-44; 53pp; English.
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                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 188; Conservative
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                                                                                                                                                                                                                                           nodgkin's disease
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N-PSDB; AAV32775.
                                                                                                                                                                                                                                                                         Sequence 222 AA;
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                                             The present claimed sequence represents a mouse glucocorticoid induced TNRR-family related protein variant B (GTR-B). The invention also claims for GITR (AAW49016) and GITR-C (AAW49018). The GITRs are claimed to be useful for stimulating lymphocyte activity and cell death rescue. GITR antagonists are claimed to be useful for suppressing the lymphocyte activity and cell man activity and for inducing apoptotic deletion. GITR cDNAs and the proteins they encode are also claimed to be useful for suppressing growth of tumour cells over-expressing GITR or for the treatment of refractory
                                                                                                                                                                                                                                                                                                                  180
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                                                                                                                                                                                                                           1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC
                                                                                                                                                                                                                                                                                                        1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC
                                                                                                                                                                                                                                                                NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL
stimulate lymphocyte activity and cell death rescue, useful to, e.g. develop products to suppress lymphocyte activity and induce apoptosis.
                                                                                                                                                                                            Gaps
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                                                                                                                                                                                          Indels
                                                                                                                                                                        Length
                                                                                                                                                                       Score 1079; DB 2;
Pred. No. 8.9e-92;
                                                                                                                                                                82.9%; Sco...
100.0%; Pred. No. co...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Therapy; cancer; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 75; 375pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cancer-associated protein, SEQ ID 75.
                             Claim 14; Page 40-41; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                                                                                                                                                                                                              ADR46662 standard; protein; 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gish KC, Wilson KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-2004; 2004WO-US005455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                            188; Conservative
                                                                                                                                                                                                                                                                                                                                        RROHMCPR 188
                                                                                                                                                                                                                                                                                                                                                          RROHMCPR 188
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                                                                                                                                                                                 Local Similarity
                                                                                                                                 hodgkin's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; Gene
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                                                                                                                                                    Sequence 294 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                        Query Match
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This is the amino acid sequence encoding the human 312C2 T cell protein. The 312C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 312C2 stimulates proliferation of T cell clones, antigen-specific proliferation
                    patient. The method comprises detecting in a biological sample from the patient a nucleotide or protein sequence comprising a sequence that is at lasts 80% identical to a nucleotide sequence (ADR46588-ADR46645) or protein sequence (ADR46646-ADR46703). The method is useful for detecting cancer for preparing a composition for diagnosing or treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                        113
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                                                                                                                                                                                                                                                                                                                                                                                                                     54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 GHCRLWTNCSOFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoietic cells; lymphoid cell;
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         227
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present invention relates to a method for detecting cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLHIWQLRRQHMCPRETQPFABVQLSAEDACSFQFPEBERGEQT-EEKCHLGGRW
                                                                                                                                                                                                                                                                     6
                                                                                                                                                                                                                         Length 240;
                                                                                                                                                                                                                                                                                                                            1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid seguence of the human 312C2 T cell protein.
                                                                                                                                                                                                                      56.5%; Score 735.5; DB 8; 57.0%; Pred. No. 5.7e-60; rative 31; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zlotnik A;
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96US-0027901P.
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                                                                                                                                                                                                                                                                             Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune disorders.
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                                                                                                                                                                                                                                                     Similarity
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cell disorders.
                                                                                                                                                                               Sequence 240 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 (
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Best Local 3
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and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells, e.g. lymphoid cells which affect immunological responses, e.g. autoimmune
                                                                                                                                                                                                                                                                       66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHE 125
                                                                                                                                                                                                                                                       54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
                                                                                                                                                                                                                                                                                                              GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
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                                                                                                                                                                                                 1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-----PGKE 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO364, tumour necrosis factor receptor; human, apoptosis; inflammation; antiinflammatory; NF-KB activation; autoimmune disease; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor necrosis factor receptor homologue - useful for, e.g. modulating
                                                                                                                                                                                                                7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEB
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                    174 GLHIWOLRROHMCPRETOPFAEVOLSAEDACSFOFPEEERGEOT-EEKCHLGGRW
                                                                                                                                           DB 2; Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood WI;
                                                                                                                                                                     Matches 134; Conservative 31; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pitti RM,
                                                                                                                                        56.5%; Score 735.5; DB 2 57.0%; Pred. No. 5.8e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162. .180
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marsters SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ....25
'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26. .241
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human TNF receptor homologue PRO364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY06605 standard; protein; 241 AA
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                                                                                                                                                        Similarity
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                                                                                                               Sequence 241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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                                                                    e.g. lymph
disorders
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                                                                                                                                           Query Match
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The present sequence represents human PRO364, a novel member of the tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the recombinant production of PRO364 polypeptides, e.g. in CHO, Escherichia coli or yeast production of PRO364 polypeptides, e.g. in CHO, Escherichia coli or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-c. the marure protein) and 26-X of the present sequence, where X is any one of amino acid respoises 157-167 of PRO364. PRO364 polypeptides are useful for modulating apoptosis, NF-KB activation comprising a PRO364 polypeptide fused to a chimmeric molecules comprising a PRO364 polypeptide fused to a charmed produce such as epitope tag or immunoglobulin Fc region are also claimed. PRO364 can be used in assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or agonists of receptor/ligand binding. The PRO364 chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W Human; immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; hademostatic; antiarthryoid; antidiabetic; nootropic; neuroprotective; antianaemic; hepatotropic; viruoide; antipsoriatic; antiallargic; antianaemic; hepatotropic; viruoide; antipsoriatic; antiallargic; wateaathritis; spondyloarthropathy; systemic sclerosis; sarcoidosis; widiopathic inflammatory myopathy; systemic sclerosis; sarcoidosis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; watoimmune thrombocytopaemia; immune-mediated renal disease; watoimmune thrombocytopaemia; immune-mediated renal disease; watoimmune disease; hepatobiliary disease; Whipple's disease; watoimmune-mediated skin disease; immune-mediated skin disease; immune-mediated skin disease; allergic disease; watturoimmune associated disease;
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apoptosis and NF-KB activation and proinflammatory or autoimmune
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.5%; Score 735.5; DB 2;
57.0%; Pred. No. 5.8e-60;
iive 31; Mismatches 61;
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                                                                 Claim 17; Fig 2A; 104pp; English
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Best Local Similarity
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Homo sapiens

gluten-sensitive enteropathy and Whipple's disease, autoimmune

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-pRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, spendyloarthropathies, systemic selected; arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune thromborytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Lu Y, Pan J, Pennica D, Shelton DL, Smith V;
Tumas D, Watanabe CK, Wood WI, Yan M;
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                                                                        9905-0123618P-
9905-0123957P-
9905-0125775P-
9906-0128843P-
9906-0131445P-
9905-0131478P-
9905-0132371P-
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99US-0144758P.
99US-0145698P.
99US-0146222P.
99WO-US020111.
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99WO-US028634.
99WO-US028551.
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99WO-US021547.
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20-APR-1999;
28-APR-1999;
04-MAY-1999;
14-MAY-1999;
02-JUN-1999;
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05-JAN-2000;
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                                                02-MAR-2000;
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                              14-SEP-2000
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02-DEC-19
02-DEC-19
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05-OCT-1
29-OCT-1
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or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AAC58379 to AAC58579 trepesent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58642 and AAB33414 to AAB33347 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                            114 GHCRIMTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL
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                                                                                                                                                                                                                        Length 241;
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                                                                                                                                                                                                                        56.5%; Score 735.5; DB 3;
57.0%; Pred. No. 5.8e-60;
ive 31; Mismatches 61;
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/note= "Asn is N-glycosylated"
156. .162
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'note= "N-myristoylation site"
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|abel= Mature_PRO364_protein
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/label= Signal_peptide
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/note= "N-
118. .124
/note= "N-
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                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                     Sequence 241 AA;
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The present invention relates to methods for stimulating or inhibiting angiogenesis and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following proteins, PRO179, PRO218, PRO344, PRO846, PRO1760, PRO205, PRO321, PRO331, PRO840, PRO877, PRO846, PRO842, PRO885 or PRO887. These proteins were identified by isolating cDNA clones encoding secreted proteins. The proteins of the invention may be used to diagnose and treat cardiovascular, endothelial or angiogenic disorders. The present sequence is one of the proteins of the invention
                                                                                                                                                     Cardiovascular; endothelial; angiogenic disorder; PRO179; PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO321; PRO833; PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; PRO887; Gene therapy.
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57.0%; Pred. No. 5.8e-60;
ive 31; Mismatches 61;
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Goddard A, Gurney AL, Hillan KJ, Marsters
Watanabe CK, Williams PM, Wood WI;
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/label= Signal peptide
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99US-0123957P.
99WO-US012252.
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                                                (first entry)
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Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC
                                                                                                    Human protein PRO364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-611444/58.
N-PSDB; AAA99903.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200053757-A2
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18-FEB-2000;
18-FEB-2000;
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Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-FEB-2000;
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30-NOV-1999;
30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAR-1999;
12-MAR-1999;
02-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2000;
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JUL-1999;
01-SEP-1999;
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                                                26-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-SEP-2000
AAB27651;
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                                                                                                                                                                                                                                                                                                                                                     Peptide
$\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\frac{1}{2}\f
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the human PRO364 protein, encoded by the CDNA clone, designated as DNA47365-1206. It is isolated from human small intestine tissue CDNA library, identified using probes based on the consensus sequence DNA4825, relative to the Incyte expressed sequence tag (EST) 3003460. This EST has homology to tumour necrosis factor receptor (TNRR) family of polypeptides. PRO364 sequence also shows homology to members of the TNR family and mouse GTR protein. This clone is assigned the ATCC deposit No: 209436. PRO364 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an especially useful for treatment of pRO655, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition useful for inhibiting neoplastic cell growth and for treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or their
                                                166. .177
/note= "Prokaryotic membrane lipoprotein lipid attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVPGFRCVACAMGTFSAGRD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-----PGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.5%; Score 735.5; DB 3; Length 241; 57.0%; Pred. No. 5.8e-60; tive 31; Mismatches 61; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillan K, Napier M,
                                                                                                                                 171. .193
/note= "Leucine zipper pattern"
                         label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gurney AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 31; Fig 4; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                            98US-0112850P.
98US-0113296P.
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Best Local Similarity 57.0°
Matches 134; Conservative
  .183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-412325/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N~PSDB; AAD01240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 241 AA;
                                                                                                                                                                                                                    WO200032778-A2
                                                   Binding-site
                                                                                                                                                                                                                                                                                                                              30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antagonists.
                                                                                                                                                                                                                                                                           08-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                               16-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen J,
                                                                                                                                      Region
Domain
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AAB27651
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Pitti RM;

Gerritsen ME; Paoni NF, F

H, SA,

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Gaps

6

DB 3; Length 241; Indels 23

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AAB27651 standard; protein; 241 AA

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Gaps

6

61; Indels

Mismatches

31;

Conservative

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134;
Matches
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like protein TR11 (see also AAY95879), a novel protein showing identity
to muritine glucocorticoid induced tumour necrosis factor receptor family-
related gene. The invention provides highly conserved TR11, TR11SV1 and
TR11SV2 proteins (see AAY95879-81), as well as vectors, host cells and
TR11SV2 proteins (see AAY95879-81), as well as vectors, host cells and
TR11SV2 proteins (see AAY95879-81), see well as vectors and/or TR11SV2
polypeptides are useful for treating, preventing, prognosis and/or
diagnosis of an immunodeficiency, X-linked agammaglobulinemia, severe combined
immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked
immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked
immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked
cumunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked
immunodeficiency (SCID), wiskott-Aldrich syndrome or X-linked
immunodeficiency (SCID), wiskott-Aldrich syndrome or X-linked
cutagonists (e.g. antibodies) are used to treat, prevent, prognose and/or
diagnose an autoimmune disease, especially rheumatoid arthritis, systemic
clupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The
polypeptides, polymcleotides and/or antibodies can be administered to
cells in vitro, ex vivo or in vivo or to a multicellular organism.
Csoluble forms of the polypeptides may also be used. Methods for screening
for agonist/antagonist compounds are also provided
                                                                         185
                                    GHCRLWINCSOFGFLIMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid arthritis.
                                                         TR11; human; tumour necrosis factor receptor-like protein; immunodeficiency; autoimmune disease; rheumatoid arthritis; immunosuppressive; antirheumatic; antiarthritic; haemostatic; dermatological; antiinflammatory; therapy; diagnosis; mutein; mutant.
                                                                                                              174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT-EEKCHLGGRW 227
                                                                                                                                        necrosis factor receptor-like protein TR11 mutein
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                                                                                                                                                                                                                                                     AAY95895 standard; protein; 241 AA
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99US-0134172P.
99US-0144076P.
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                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                           Human tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben SM,
                                      114
                                                                                                                                                                                                                                                                                           AAY95895;
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AAY95895
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Score 735.5; DB 3; Length 241; Pred. No. 5.8e-60;

56.5%;

Query Match Best Local Similarity

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Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
                                                                                                                                                                                           173
                                                                                                                                                                                                                                          185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, PRO, promotion, inhibition, angiogenesis, cardiovascularisation, diagnosis, trauma, wound, cancer, atherosclerosis, cardiac hypertrophy; angiogenic, proliferative, cardiant, cardiovascular, antiatherosclerotic, cytostatic, gene therapy, vaccine.
                                                                                                                                          125
                                                                                           54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
53
                                              65
                                                                                                                        GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL
                                                                                                                                                                                                                     MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-----PGKE
                                                                                                                                                                                                                                                                                               GLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEBERGEQT-EEKCHLGGRW 227
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Kuo SS, Paoni NF;
                                                                                                                                                                                                                                                                                                                         Gerber H,
Klein RD,
Wood WI;
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I, Gurney AL,
Williams PM,
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99US-0131445P.
99US-0134287P.
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99US-0162506P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J, Baker KP,
Godowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goddard A, Godomers V. Watanabe CK,
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N-PSDB; AAA77604.
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14-MAY-1999;
02-JUN-1999;
23-JUN-1999;
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26-JUL-1999;
01-SEP-1999;
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12-JAN-1999;
08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-NOV-1999;
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13-SEP-1999
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18-JAN-2001

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useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antegonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA7721 and AAB34388 to AAB34435 represent nucleotide and protein sequences used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 GHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO364; human; glucocorticoid-induced tumor necrosis factor; receptor; human indiand; hGITRL; RRO175; tumour necrosis factor receptor; TNFR; human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy; myocardial infarction; PGF 2alpha; trauma; cancer; angiogenesis; age-related macular degeneration; antibody; periodontal disease; vascular-related drug targeting; atherosclerosis; hypertension; inflammatory vascultides; Reynaud's disease; aneurysm; arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver; fibrosis; neuropathy; rheumatoid arthritis.
                                                     The present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-----PGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE
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                                                                                                                                                                                                                                                                                                                                                                                 Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Potential transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                               56.5%; Score 735.5; DB 3;
57.0%; Pred. No. 5.8e-60;
tive 31; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .26
/note= "Potential signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB47054 standard; protein; 241 AA
                 72; Fig 44; 315pp; English
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Best Local Similarity 57.09
Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                           present invention
                                                                                                                                                                                                                                                                                                                                               Sequence 241 AA;
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                 Claim
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This sequence represents PRO364 polypeptide, which is a human glucocorticoid-induced tumor necrosis factor receptor (hGITR). The corresponding ligand (hGITRL), PRO175, is given in ABB47056. PRO364 and PRO175 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiostatic disorder. The PRO364 CDNA sequence Related from an expressed sequence tag (BST) database as having completed from an expressed sequence was isolated from an expressed sequence was isolated from a library of completed from members of the tumour necrosis factor receptor (TMRR) family of polypeptides. The PRO175 CDNA sequence was isolated from a library of complete fargments derived from human umbilical vein endothelial cells completed from the prosence of completed by procardial infarction and characterized by PRO175 or their antagonists is useful for treating cardiac hypertrophy (which is an elevated level of PGF Zalpha), trauma, a cancer, or age-related can elevated level of PGF Zalpha), trauma, a cancer, or age-related macular degeneration in a human. Administering a therapeutically continibiting angiogenesis induced by PRO364 or PRO175, or their cinhibiting angiogenesis induced by PRO364 or PRO175, or their cinhibiting angiogenesis induced by PRO364 or PRO175, or their contention inflammatory vascular-related fung targeting or as therapeutic targets for the treatment or PRO175, or their arternation and treatment or Invertible of Agease, attraction and treatment of lung or liver fibrosis, periodontal diseases, attraction of bone-forming cells, central and peripheral confidence of the proventices and returning calls, central and peripheral confidence of the proventice 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173
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                                                                                                                                                                                                                                                                                                                                 Composition for diagnosing and treating cardiovascular, endothelial and angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 GHCRLWINCSQFGFLIMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQL
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                                                                                                    99US-0143304P
                                                 11-JUL-2000; 2000WO-US018867
                                                                                                                                                                                                         Williams PM, Gerritsen ME,
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                                                                                                                                                      (GETH ) GENENTECH INC
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INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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amino acid
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Best Local Similarity
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Sequence 191, App
Sequence 191, App
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                                                                  , Search time 28.6823 Seconds
(without alignments)
593.397 Million cell updates/sec
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Sequence 4, Ap
Sequence 28, A
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Sequence 8,
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1301
1 MGAWAMLYGVSWLCVLDLGQ......PEEERGEQTEEKCHLGGRWP 228
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Sequence 7,
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1. /cgn2 6/ptodata1/iaa/5A_COMB.pep:*

2. /cgn2 6/ptodata1/iaa/5B_COMB.pep:*

3. /cgn2 6/ptodata71/iaa/6A_COMB.pep:*

3. /cgn2 6/ptodata71/iaa/6B_COMB.pep:*

3. /cgn2 6/ptodata71/iaa/PCTUS_COMB.pep:*

3. /cgn2 6/ptodata71/iaa/PCTUS_COMB.pep:*

3. /cgn2 6/ptodata71/iaa/PCTUS_COMB.pep:*

3. /cgn2 6/ptodata71/iaa/PCTUS_COMB.pep:*
    GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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-09-949-016-7232
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-09-312-283C-191
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S-09-512-363-6
S-09-116-200-6
S-09-915-593-6
S-08-911-423-8
S-09-512-363-4
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-09-512-363-2
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Sequence 7520, Ap
Sequence 2, Appli
Sequence 6, Appli
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Patent No. 6111090
GENERAL INFORMATION:
APPLICANT: Gorman, Daniel M.
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: RAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAX Research Institute
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US-09-573-986-11

US-09-578-764A-2

US-09-623-545A-2

PCT-US96-03965-8

US-09-949-016-7520

US-08-816-065-2

US-08-150-864A-6

US-09-150-864A-6

US-09-150-864A-6

US-08-073-545A-3

PCT-US96-03965-2

US-08-974-022-52

US-08-974-186-52

US-08-974-186-52

US-08-974-186-52

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US-08-974-186-52

US-08-974-186-52

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US-08-974-186-52

US-08-978-186-52

US-08-978-186-52

US-08-978-186-52
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IN PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911,423

FILING DATE: 14-AUG-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: US 60/023,419

FILING DATE: 16-AUG-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/027,901

FILING DATE: 07-OCT-1996

ATTORNEY AGENT INFORMATION:

NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090

REGISTRATION NUMBER: DX0612K

TELECOMMUNICATION INPORMATION:

TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: DNAX Research Institute 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 901 Califor
CITY: Palo Alto
STATE: California
COUNTRY: USA
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Length 228;

Score 1301; DB 3; Pred. No. 1.8e-121;

100.0%;

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Sequence 7, Application US/09915593
Patent No. 6689607
GENERAL INFORMATION:
                                     APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M.
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LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT; ORGANISM: Mus musculus
US-09-915-593-7
                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Mus musculus
US-09-176-200-7
                      GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FACULANT INFORMATION:
APPLICANT Ni, Jian
APPLICANT Ruben, Steven M.
APPLICANT Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: TR11, TR115V1, and TR115V2
FILE REFERENCE: PF396
CURRENT APPLICATION NUMBER: US/09/512,363
CURRENT APPLICATION NUMBER: 06/063,212
EARLIER FILING DATE: 1997-10-21
EARLIER PLING DATE: 1998-10-21
EARLIER PLICATION NUMBER: 60/176,200
EARLIER PLICATION NUMBER: 60/116,200
EARLIER PLICATION NUMBER: 60/134,172
EARLIER FILING DATE: 1999-05-13
EARLIER PILING DATE: 1999-05-13
EARLIER FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 28

NUMBER OF SEQ ID NOS: 28
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                                                                              1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
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Gaps
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0; Mismatches
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US-09-176-200-7
Sequence 7, Application US/09176200
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Patent No. 6503184
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  Matches
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121 NCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQL 180
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APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: TRII, TRAILSV1, and TRIISV2
FILE REFERENCE: PF396P2
CURRENT APPLICATION NUMBER: US/09/915,593
CURRENT APPLICATION NUMBER: US/0221,577
PRIOR APPLICATION NUMBER: 60/221,577
PRIOR APPLICATION NUMBER: 60/121,577
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 2000-07-16
PRIOR PILING DATE: 1999-05-13
PRIOR PILING DATE: 1999-05-13
PRIOR PILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-10-21
PRIOR FILING DATE: 1997-10-21
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TITLE OF INVENTION: Human Tunor Necrosis Factor Receptor-Like Proteins TITLE OF INVENTION: TRI1, TRI1SV1, and TRI1SV2
TITLE OF INVENTION: TRI1, TRI1SV1, and TRI1SV2
TITLE OF INVENTION: TRI1, TRI1SV1, and TRI1SV2
CURRENT APPLICATION NUMBER: US/09/176,200
CURRENT FILING DATE: 1998-10-21
EARLIER APPLICATION NUMBER: 60/063,212
EARLIER FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 27
SOFTWARES PATENTIN Ver. 2.0
SEQ ID NO 7
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC
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100.0%; Score 1301; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.8e-121;
Matches 228; Conservative 0; Mismatches 0;
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RESULT 7
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                                                                                                     1 MGAWAMLYGVSWLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 60
                                                                                                                                                                                    61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT
                                                                             1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC
                                           Gaps
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APPLICANT: Gorman, Daniel M.
APPLICANT: Randall,
APPLICANT: Zlocinik, Albert
TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAK Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 241;
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Length 228;
                                      0; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
CLASSIFICATION NUMBER: US/08/911,423
FILING APPLICATION DATA:

APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION NUMBER: US 60/027,901
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: CAING: GAWIN P.

REGISTRATION NUMBER: 34,090
REFERENCE/POCKET UNMBER: 34,090
REFERENCE/POCKET UNMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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57.0%; Pred. No. 3.1e-65;
tive 31; Mismatches 61;
Query Match 100.0%; Score 1301; DB 4; Best Local Similarity 100.0%; Pred. No. 1.8e-121; Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08911423
Patent No. 6111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 57.0%
Matches 134; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Sequence 28, Application US/09512363

Sequence 28, Application US/09512363

Patent No. 6503184

GENERAL INCPORMATION:
APPLICANT: Nuben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
FILE REFERENCE: PF396
CURRENT APPLICATION NUMBER: US/09/512,363
CURRENT FILING DATE: 1997-10-21
EARLIER PILING DATE: 1997-10-21
EARLIER FILING DATE: 1998-10-21
EARLIER FILING DATE: 1998-10-21
EARLIER FILING DATE: 1998-05-13
EARLIER FILING DATE: 1999-05-13
EARLIER FILING DATE: 1999-05-13
EARLIER FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOWSER: 60/134,172
EARLIER FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 28
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                                                        Gaps
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1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA--
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US-09-512-363-28
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, MOLECULE TYPE: peptide US-08-911-423-6
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STRANDEDNESS: sin
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ORGANISM: Human
     ; OKSANAS...
US-09-949-016-7232
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TILLE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PLING DATE: 2000-04-14
PRIOR PLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FLING DATE: 2000-10-03
PRIOR RELING DATE: 2000-09-08
PRIOR RELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTWARE: FRACES for Windows Version 4.0
SEQ ID NO 7232
TYPE: PRI
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                                 APPLICANT: NJ, Usan
APPLICANT: NJ, Usan
APPLICANT: NJ, Usan
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: Human Tumor Necrosis Factor
TITLE OF INVENTION: TR11, TR11SV1, and TR11SV2
FILE REFERENCE: PF396F2
CURRENT FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: 09/512,363
PRIOR APPLICATION NUMBER: 09/512,363
PRIOR PILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-16
PRIOR PELING DATE: 1999-02-24
PRIOR PILING DATE: 1999-02-24
PRIOR PLING DATE: 1999-10-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7232, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-593-28
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                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08911423
; Sequence 6, Application US/08911423
; Patent No. 6111090
; GENERAL INPORMATION:
APPLICANT: Randall, Troy D.
APPLICANT: Zlotnik, Albert
TILLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
TITLE OF INVENTION: REAGENTS
; TITLE OF INVENTION: REAGENTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
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                                                                                                  1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA---
  Length 241;
                                                  Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: ELOppy disk
COMPUTER: PLOppy disk
COMPUTER: Day PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/911,423
FILING DATE: 14-AUG-1997
  DB 4;
56.5%; Score 735.5; DB 4 57.0%; Pred. No. 3.1e-65;
                       Best Local Similarity 57.0%; Pred. No. 3.1e-
Matches 134; Conservative 31; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,419
FILING DATE: 16-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/027,901
FILING DATE: 07-0CT-1996
ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: DX0612K
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 228 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-09-915-593-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ni, Jian
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: TRII, TRIISVI, and TRIISV2
FILE REFERENCE: PF396
CURRENT APPLICATION NUMBER: US/09/512,363
CURRENT FILING DATE: 2000-02-23
EARLIER APPLICATION NUMBER: 06/063,212
EARLIER FILING DATE: 1997-10-21
EARLIER FILING DATE: 1998-10-21
EARLIER FILING DATE: 1999-02-24
EARLIER FILING DATE: 1999-05-13
EARLIER FILING DATE: 1999-05-13
EARLIER FILING DATE: 1999-05-13
EARLIER FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 2
LENGTH: 234
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                                                                                             16; Gaps
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DB 3; Length 228,
Query Match 54.0%; Score 703; DB 3; Length 228
Best Local Similarity 54.9%; Pred. No. 5e-62;
Matches 129; Conservative 32; Mismatches 58; Indels
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ORGANISM: Homo sapiens
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Sequence 2, Application US/09915593

patent No. 6689607

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US-09-176-200-2
; Sequence 2, Application US/09176200
; Patent No. 6509173
; GENERAL INFORMATION:
; APPLICANT: NI, Usen
; APPLICANT: NI, Usen
; TITLE OF INVENTION: TRIL; TRILSVL, and TRILSV2
; TITLE OF INVENTION: TRIL; TRILSVL, and TRILSV2
; TITLE REPRENCE: PP396
; CURRENT APPLICATION NUMBER: US/09/176,200
; CURRENT PILING DATE: 1998-10-21
; BARLIER PILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 27
; NUMBER OF SEQ ID NOS: 27
; SOFTHARE: PatentIn Ver: 2.0
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SEQ ID NO 2
LENGTH: 234
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Matches 129, Conservative
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Query Match
Best Local Similarity 52.2%
Matches 129; Conservative
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                     221 CHLGGRW 227
                                                                    233 GRĽĠDĽW 239
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US-09-915-593-6
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; Sequence Application US/09512363
; Patent No. 6503184
; GENERAL INFORMATION:
    APPLICANT: Ni, Jian
; APPLICANT: Ruben, Seeven M.
    TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
; TITLE OF INVENTION: TRII, TRIISV1, and TRIISV2
; TITLE OF INVENTION: HUMBER: US/09/512,363
; CURRENT FILING DATE: 1090-10-21
; EARLIER PILING DATE: 1997-10-21
; EARLIER PILING DATE: 1999-02-24
; EARLIER PILING DATE: 1999-05-13
; EARLIER PILING DATE: 1999-05-13
; EARLIER PILING DATE: 1999-05-13
; EARLIER PILING DATE: 1999-07-16
; RARLIER PILING DATE: 1990-07-16
; RARLIER PILING DATE: 1990-07-16
; RARLIER PAPELCATION NUMBER: 60/144,076
; RARLIER PAPELCATION NOWS: 20
; SEQ ID NOS : 28
; SEQ ID NOS : 20
; SEQ ID NOS : 20
; SEQ ID NOS : 20
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                                                                      Length 234;
                                                                 Query Match 54.0%; Score 703; DB 4; Length 23 Best Local Similarity 54.9%; Pred. No. 5.2e-62; Matches 129; Conservative 32; Mismatches 58; Indels
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Matches 129; Conservative
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ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-915-593-2
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Sequence 6, Application US/09176200
; Sequence 6, Application US/09176200
; Patent No. 6509173
; GENERAL INFORMATION:
    APPLICANT: Ni, Jian
    APPLICANT: Ruben, Steven M.
    TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
    TITLE OF INVENTION: TR11, TR115V1, and TR115V2
    TITLE REFERENCE: PF396
; CURRENT APPLICATION NUMBER: US/09/176,200
; CURRENT FILING DATE: 1998-10-21
; EARLIER PILLING DATE: 1997-10-21
; NUMBER OF SEQ ID NOS: 27
; SOFTHARE: PatentIn Ver. 2.0
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180 AACVLLLTSAQLGLHIWQLRK-----TQLLLEVPPSTEDARSCQFPEEERGERSAEEK 232
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APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: TRIL, TRILSVI, and TRILSV2
FILE REFERENCE: PF396P2
CURRENT PEPLICATION NUMBER: US/09/915,593
CURRENT FILING DATE: 2000-07-27
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 2000-02-23
PRIOR PLING DATE: 2000-02-23
PRIOR PLING DATE: 2000-07-16
PRIOR PLING DATE: 1090-07-16
PRIOR FILING DATE: 1090-05-13
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PRIOR FILING DATE: 1999-02-24
PRIOR PRILING DATE: 1999-02-24
PRIOR PILING DATE: 1999-10-21
PRIOR FILING DATE: 1997-10-21
PRIOR PILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 6
LENGTH: 240
LENGTH: 240
TYPE: PRT
ORGANISM: Homo sapiens
US-09-915-593-6
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1301
1 MGAWAMLYGVSMLCVLDLGQ......PEEERGEQTEEKCHLGGRWP 228
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5: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/USO0_PUBCOMB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1862994 seqs, 417510619 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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מסידיייססמ	neart there	Sequence 7, Appli	Sequence 24, Appl	Sequence 7, Appli	Sequence 7, Appli	Sequence 24, Appl	Sequence 75, Appl	Sequence 28, Appl	Sequence 3, Appli	Sequence 28, Appl	Sequence 28, Appl	Sequence 1284, Ap
f		US-09-915-593-7	US-10-116-378-24	US-10-283-105-7	US-10-277-966-7	US-10-959-537-24	US-10-783-528-75	US-09-915-593-28	US-10-116-378-3	US-10-283-105-28	US-10-277-966-28	US-10-295-027-1284
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Suery	Length	228	228	228	228	228	240	241	241	241	241	241
Query	March	100.0	100.0	100.0	100.0	100.0	56.5	56.5	56.5	56.5	56.5	56.5
	Score	1301	1301	1301	1301	1301	735.5	735.5	735.5	735.5	735.5	735.5
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735.5 56.5 241 1703 54.0 234 4 1703 54.0 234 4 1703 54.0 234 4 1703 54.0 234 4 1703 54.0 234 4 1705 23.6 240 1705 23.6 240 1705 23.6 240 1705 23.6 240 1705 23.6 240 1705 23.6 240 1705 23.6 240 1705 23.6 240 1705 23.6 240 1705 23.6 240 1705 23.6 240 1705 23.6 240 1705 23.6 23.0 23.0 23.0 23.0 23.0 23.0 23.0 23.0
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ALIGNMENTS

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NESCULT 1

Sequence 7, Application US/09915593

SENERAL INFORMATION: Human Tumor Necrosis Factor Receptor-Like Proteins

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins

TITLE OF INVENTION: TRIL; TRILSV1, and TRILSV2

CURRENT APPLICATION NUMBER: US/09/915,593

CURRENT FILING DATE: 2000-07-28

PRIOR FILING DATE: 2000-07-28

PRIOR PLING DATE: 2000-07-28

PRIOR PLING DATE: 1999-05-23

PRIOR PLING DATE: 1999-05-23

PRIOR PLING DATE: 1999-05-24

PRIOR PLING DATE: 1999-05-24

PRIOR PLING DATE: 1999-10-21

PRIOR PLING DATE: 1998-10-21

PRIOR FILING DATE: 1997-10-21

PRIOR FILING DATE: 1998-10-21

PRIOR FILING DATE: 1998-10-21

PRIOR FILING DATE: 1998-10-21

PRIOR FILING DATE: 1997-10-21

PRIOR FILING DATE: 1999-10-21

PRIOR FILING DATE: 1999-10-2
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US-10-277-966-7
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Sequence 24, Application US/10116378

Publication No. US20020150993A1

SEQUENCE No. US20020150993A1

SERENTAL INFORMATION:

APPLICANT: Goddard, Audrey

APPLICANT: Gurney, Austin

APPLICANT: Gurney, Austin

APPLICANT: Pitti, Robert M.

CURRENT: PILIGE DE INVENTION: NUCLEIC

TITLE OF INVENTION: NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P1206R1

CURRENT FILING DATE: 2002-04-04

CURRENT FILING DATE: EARLIER FILING DATE: 1999-02-09

PRIOR PILING DATE: EARLIER FILING DATE: 1999-02-09

PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09

SEQ ID NO 24

LEMICH: 228

TYPE: DATE: 228
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  DB 9; Length 228;
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                                                  Indels
Query Match 100.0%; Score 1301; DB 9; Best Local Similarity 100.0%; Pred. No. 2.3e-114; Matches 228; Conservative 0; Mismatches 0;
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Sequence 7, Application US/10283105
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Best Local Similarity 100.0
Matches 228; Conservative
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US-10-116-378-24
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APPLICANT: Ni, Jian
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
TITLE OF INVENTION: TR11SV2
FILE REFERENCE: PF396FD10
CURRENT APPLICATION NUMBER: US/10/277,966
CURRENT FILING DATE: 2002-10-23
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
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Publication No. US20030153499A1
GENERAL INFORMATION:
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US-10-783-528-75
) Sequence 75, Application US/10783528
; Publication No. US20040219579A1
; GENERAL INFORMATION:
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US-10-783-528-75
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US-09-915-593-28
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LENGTH: 240
TYPE: PRT
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                                                                                                                                                                                                   Score 1301; DB 14; Length 228; Pred. No. 2.3e-114;
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100.0%; Pred. No. ...
0; Mismatches
PRIOR FILING DATE: 1999-05-13
PRIOR PLING DATE: 1999-05-13
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 09/176,200
PRIOR APPLICATION NUMBER: 09/176,200
PRIOR APPLICATION NUMBER: 60/063,212
PRIOR PILING DATE: 1997-10-21
NUMBER: 05 SEQ ID NOS: 28
SOFTWARE: PALENTIN VETSION 3.1
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Best Local Similarity 100.C
Matches 228; Conservative
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Best Local Similarity 100.0
Matches 228; Conservative
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US-10-959-537-24
                                                                                                                                                 TYPE: PRT
ORGANISM: mouse
US-10-277-966-7
                                                                                                                                     LENGTH: 228
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s Sequence 28, Application US/09915593
s Patent No. US20020098525A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: Human Tumor Necrosis Factor
TITLE OF INVENTION: 000-07-27
CURRENT APPLICATION NUMBER: 2001-07-27
PRIOR APPLICATION NUMBER: 60/221,577
PRIOR PLILNG DATE: 2000-07-28
PRIOR PLILNG DATE: 2000-02-23
PRIOR PLILNG DATE: 2000-07-28
PRIOR PLILNG DATE: 2000-07-16
PRIOR FILING DATE: 1999-05-13
                                                                                                 121 NCSOFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVWAACIFFLTTVQLGLHIWQL 180
61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
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APPLICANT: Gish, Kurt
APPLICANT: Gish, Kurt
APPLICANT: Gish, Kurt
APPLICANT: Gish, Kurt
APPLICANT: John, Keith
TITLE CANT: Zlotnik, Albert
TITLE OF INVENTION: METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND
FILE REFERENCE: 05882.0191.NPUSO1
CURRENT APPLICATION NUMBER: US/10/783,528
CURRENT FILING DATE: 2004-02-19
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PATENTIN VERSION 3.2
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                                                                                                                                                                                                                                      Query Match

56.5%; Score 735.5; DB 16; Length

Best Local Similarity 57.0%; Pred. No. 5e-61;

Matches 134; Conservative 31; Mismatches 61; Indels
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RESULT 10
US-10-277-966-28
; Sequence 28, Application US/10277966
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CURRENT APPLICATION NUMBER: US/10/116,378
CURRENT FILING DATE: 2002-04-04
PRIOR PILING DATE: EARLIER APPLICATION NUMBER: 09/247,225
PRIOR PILING DATE: EARLIER FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
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                                                                                                                                                                                                                                                                                   Length 241;
                                                                                                                                                                                                                                                                56.5%; Score 735.5; DB 9; Leuyun. 57.0%; Pred. No. 5e-61; uicmatches 61; Indels
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PRIOR APPLICATION NUMBER: 60/121,030
PRIOR FILING DATE: 1999-02-24
PRIOR PELING DATE: 1999-02-24
PRIOR PILING DATE: 1999-10-21
PRIOR PILING DATE: 1998-10-21
PRIOR APPLICATION NUMBER: 60/063,212
PRIOR APPLICATION NUMBER: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marsters, Scot A. APPLICANT: Pitti, Robert M. APPLICANT: Wood, William
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APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
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Best Local Similarity 57.0%
Matches 134; Conservative
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 57.09
Matches 134; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
TITLE OF INVENTION: TR11Sv22
FILE REFERENCE: PF396P3
CURRENT APPLICATION NUMBER: US/10/283,105
CURRENT FILING DATE: 2002-10-30
66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
                                                                                            54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD 113
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PRIOR APPLICATION NUMBER: 60/330,757
PRIOR FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/915,593
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 1000-02-33
PRIOR APPLICATION NUMBER: 60/144,076
PRIOR APPLICATION NUMBER: 60/134,172
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: 60/134,172
PRIOR FILING DATE: 1999-02-14
PRIOR FILING DATE: 1999-02-14
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 28
SOFFWARE: PATCHTIN VERSION 3.1
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Sequence 28, Application US/10283105; Publication No. US20030138426A1
GENERAL INFORMATION:
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Millian
APPLICANT: Mood, Willian
TILLE OF INVENTION: NOVEL M.
APPLICANT: Wood, Willian THMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P1206R1
CURRENT APPLICATION NUMBER: US/10/959,537
CURRENT FILING DATE: 1999-02-09
PRIOR PLILING DATE: 1999-02-09
PRIOR PLILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 3
LENGTH: 241
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PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-11-21
PRIOR PILING DATE: 2001-11-24
PRIOR PLING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-08
PRIOR PILING DATE: 2002-01-10
PRIOR PILING DATE: 2002-01-13
PRIOR PILING DATE: 2002-02-08
PRIOR PILING DATE: 2002-02-03
PRIOR PILING DATE: 2002-02-03
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Best Local Similarity 57.0%; Pred. No. 5e-61;
Matches 134; Conservative 31; Mismatches 61; Indels 9;
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; ORGANISM: Homo sapiens
US-10-959-537-3
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US-10-295-027-1284
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                                                                        APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
TITLE OF INVENTION: TR11SV2
FILE REFERENCE: PF396P1D1
CURRENT APPLICATION NUMBER: US/10/27,966
CURRENT FILING DATE: 2000-20-23
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-34
PRIOR PELICATION NUMBER: 60/121,648
PRIOR FILING DATE: 1999-05-13
PRIOR PELICATION NUMBER: 60/134,172
PRIOR PELICATION NUMBER: 60/144,076
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR PELING DATE: 1999-10-21
PRIOR PELING DATE: 1999-10-21
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TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFREEMENCE: 018501-012500UG
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
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Publication No. US20030232350A1
GENERAL INFORMATION:
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Giah, Kutt C.
Glynne, Richard
Hevezi, Peter A.
Mack, David H.
Murray, Richard
Watson, Susan R.
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APPLICANT: Aziz, Natasha
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CRGANISM: human
US-10-277-966-28
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                                                                                                     1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-----PGKE
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APPLICANT: P. Mickey Williams
APPLICANT: P. Mickey Williams
TITLE OF INVENTION: PROMOTION OR INHIBITION OF ANGIOGENESIS AND
TITLE OF INVENTION: CARDIOVASCULARIZATION BY TUMOR NECROSIS FACTOR
TITLE OF INVENTION: LIGAND/RECEPTOR HOMOLOGS
TITLE OF INVENTION: LIGAND/RECEPTOR HOMOLOGS
TITLE OF INVENTION: LIGAND/RECEPTOR HOMOLOGS
TITLE OF INVENTION: UNMBER: US/11/032,294
CURRENT APPLICATION NUMBER: US/11/032,294
CURRENT FILING DATE: CURRENT APPLICATION NUMBER: US/09/613,972
PRIOR APPLICATION NUMBER: US 60/143,304
PRIOR FILING DATE: 1999-07-12
NUMBER OF SEQ ID NOS: 22
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                  DB 17; Length 241;
           56.5%; Score 735.5; DB 17; Length
57.0%; Pred. No. 5e-61;
tive 31; Mismatches 61; Indels
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Publication No. US20050202008A1
Query Match
Best Local Similarity 57.0%
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Sequence 2, Application US/09915593 Patent No. USZ00200098525A1 GENERAL INFORMATION: APPLICANT: Ni, Jian

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APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
TITLE OF INVENTION: P396P3
TITLE OF INVENTION: P4016 P302-10-30
FILE REFERENCE: P5396P3
CURRENT PAPLICATION NUMBER: 06/330,757
PRIOR FILING DATE: 2001-00-30
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-05-13
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APPLICANT: Ruben, Steven M.

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: TR11, TR118V1, and TR118V2
FILE REFERENCE: PF396P2
CURRENT APPLICATION NUMBER: US/09/915,593
CURRENT FILING DATE: 2001-07-27
PRIOR PPLICATION NUMBER: 09/21,577
PRIOR APPLICATION NUMBER: 09/512,363
PRIOR PLING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/144,076
PRIOR PLING DATE: 2000-07-16
PRIOR PLING DATE: 1999-05-13
PRIOR PLING DATE: 1999-05-13
PRIOR PLING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-14
PRIOR PLING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN VEY: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/10283105; Publication No. US20030138426A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 54.9%
Matches 129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-283-105-2
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1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-----PGKE 53
                                                                                                                                                                                                                                                                  Query Match
54.0%; Score 703; DB 14; Length 234;
Best Local Similarity 54.9%; Pred. No. 5.6e-58;
Matches 129; Conservative 32; Mismatches 58; Indels 16; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/121,648
PRIOR FILING DATE: 1999-02-24
PRIOR APPLICATION NUMBER: 09/176,200
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 234
                                                                                                                                      ; TYPE: PRT
; ORGANISM: human
US-10-283-105-2
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Search completed: October 26, 2005, 16:11:20 Job time : 111.382 secs

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- protein search, using sw model OM protein

Run on:

October 26, 2005, 15:38:30; Search time 24.307 Seconds (without alignments) 902.513 Million cell updates/sec

US-09-545-998B-2 1301 Title: Perfect score:

1 MGAWAMLYGVSMLCVLDLGQ.......PEEERGEQTEEKCHLGGRWP 228 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	lymphocyte activat	T-cell antigen 4-1	gene ox40 protein	OX40 antigen precu	Ä	OX40 homolog - hum	low-density lipopr	B-cell activation	tumor necrosis fac	gene murine tumour	tumor necrosis fac	B cell-associated	tumor necrosis fac	protein-tyrosine k	alpha-2-macroglobu	p-185 precursor -	notch3 protein - h	CD27 antigen precu	death receptor-6 -	laminin beta-2 cha	egr		latent transformin	scavenger receptor	ď	-	ă	æ	insulin-like growt
COLUMNIES		92	93	00	83	53	52	15	71	82	54	34	94	26	NG DN	02	61	49	17	05	77	50	59	93	61	01	41	94	53	805
ñ	Ð	138426	B32393	I48700	S12783	A49053	137552	JE0315	A60771	154182	148854	B38634	A46476	A35356	TVRTNU	A53102	148161	878549	A46517	JC7705	A55677	JC7850	T09059	A57293	JC4361	A27701	A32141	I45894	0	A488
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æ	Ouery Match	17.6	ഗ	10.3	9.7	9.6	9.4	9.1	9.1	8.8	8.3	8.5	8.0	7.9	7.9	7.9	7.7	7.7	7.7	7.6	7.6	7.6	7.6	7.5	7.3	7.3	7.3	7.3	7.3	7.3
	Score	228.5	203.5	134	126.5	125.5	122	119	118.5	115	107.5	106.5	104.5	102.5	102.5	102.5	100.5	100.5	100	99.5	99.5	66	66	96	95.5		95	95	95	94.5
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hypothetical prote alpha-2-macroglobu	lectin precursor - follistatin - shee	follistatin - chic oocyst wall protei	insulin-like growt	periecan precursor lectin-B - Virgini	follistatin - mous	hypothetical prote	gene serrace proce mucin - rat	notch 3 protein -	P-selectin - rat	epidermal growth r
T16840 S25111	LNRZ 147079	S55369 S36016	A33837	A38096 JC5559	845321	T34513	S16148 JC5598	845306	153821	EGMSMG
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30	333	3.4 4.4	36	37	36	40	4 4 2 2	43	44	45

ALIGNMENTS

RESULT 1
I38426
lymphocyte activation-induced receptor ILA precursor - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C; Accession: I38426; JT0752
R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Fal
Eur. J. Immunol. 24, 2219-2227, 1994
A:Title: Molecular and biological characterization of human 4-1BB and 1ts ligand
A; Reference number: 138426; MUID: 94374434; PMID: 8088337
A; Accession: 138426
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

1k, B.; Rc

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A,Rolecule 1.255 cRES.
A,Cross-references: UNIPROT:Q07011; EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g57133;
R,Schwarz, H.; Tuckwell, J.; Lotz, M.
R,Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
A,Title: A receptor induced by lymphocyte activation (ILA): a new member of the human ner
A,Reference number: J70752
A,Accession: J70752
A,Rolecule type: mRNA
A,Residues: 1-106, "R':108-255 <SCH>
C,Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necros
C,Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necros
C,Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necros
C,Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necros
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C,Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necros
C,Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necros
C,Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necros
C,Comment: This protein plosphorotein; receptor repeat homology
C,Reywords: glycoprocein; phosphorotein; receptor; transmembrane protein
F,1-17/Domain: signal sequence #status predicted F,180,149/Binding site: phosphate (Thr) (covalent) #status predicted
F,234,235/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted
F,242/Rinding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F,242/Rinding site: phosphate (Ser) (covalent) (By protein kinase C) #status predicted
F,242/Rinding site: Phosphate (Ser) (covalent) (By protein kinase C) #status predicted
F,242/Rinding site: Phosphate (Ser) (covalent) (By protein kinase C) #status predicted
F,242/Rinding site: Phosphate (Ser) (covalent) (By protein kinase C) #status predicted
F,242/Rinding site: Phosphate (Ser) (covalent) (By Pasein kinase C) #status predicted
F,242/Rinding Site: Pasein kinase C) #statu

10; Gaps 55; 17.6%; Score 228.5; DB 2; Length 255; 27.2%; Pred. No. 7.5e-12; tive 30; Mismatches 97; Indels 55. Query Match Best Local Similarity 27.29 Matches 68; Conservative

46

-----RCGPGKVQNGSGNNT-----RCCS

11 SMLCVLDLGQPSVVEEP----

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47 LYAPGKE--DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACA 104 ::| | | : :::| | | : ::| | 1 | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : В ઠે 셤

122 FGTFNDQKRGICRPWTNCSLDGKSVLVNGTKERDVVCGPSPADLSPGASSVTPPAPAREP 181 -----PLPTEQY 151 105 MGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPE----q

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Willermate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Saper-139-56p-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S12789; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Fitle: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes
A;Reference number: S12783; MUID:90214614; PMID:2157591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Accession: S12783
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Cross-references: UNIPROT: P15725, EMBL: X17037; NID: 957830; PIDN: CAA34897.1; PID: 957831
C, Superfamily: CD27 antigen; NGF receptor repeat homology
C, Superfamily: CD27 antigen; NGF ransmembrane protein
F, 1-19/Domain: signal sequence #status predicted < SIG>
F, 20-271/Product: OX40 antigen #status predicted < MAT>
F, 211-235/Domain: transmembrane #status predicted < TMM>
                                                                                 rat OX40
R;Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N. Eur. J. Immunol. 25, 926-930, 1995
A;Title: Gene structure and chromosomal localization of the mouse homologue of A;Reference number: 148334; WUID:95255413; PMID:7737295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 SQGDIVFGFRCVACAMGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVC----- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55 TRDTLCHPCETGFYNEAVNYDTC--KQCTQCNHRSGSELKQNCTPTQDTVCRCRPGTQPR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 ODSGYKLGVDCVPCPPGHFSPGNNQACKPWTNCTLSGKQTRHPASDSLDAVCEDRSLLAT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 LLWETQRPTFRPTTVQSTTVWPRTSELPSP-PTLVTPEGPAFAVLLGLGLGLLAPLTVLL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 TRDIVCHPCEPGFYNEAVNYDIC--KQCIQCNHRSGSELKQNCIPTEDIVCQCRPGIQPR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGK---EDCPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGK---BDCPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MYVWVQQPTAFLLLGLSLG----VTVKLNC----VKDTYPSGHKCCRECQPGHGMVSRCDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MYVWVQQPTALLLLALTLG--VTARRLNC----VKHTYPSGHKCCRECQPGHGMVSRCDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 ER---C-ICVTPEYH-----CGDPQCKICKHYP------CQPGQRVE
                                                                                                                                                                                A,Status: translated from GB/EMBL/DDBJ
A,Moblecule type: DNA
A,Residues: 1-14,'G',16-272 <RE2>
A,Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.7%; Score 126.5; DB 2; Length 271;
llarity 21.6%; Pred. No. 0.0024;
Conservative 27; Mismatches 105; Indels 93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 SOGDIVFGFRCVACAMGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 GLHIWQLRRQHMCPRETQPFAEVQLSAEDAC---SFQFPEEERGEQTE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.3%; Score 134; DB 2; Length 272; Best Local Similarity 22.9%; Pred. No. 0.00057; Matches 66; Conservative 25; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OX40 antigen precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
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                                                                                                                                                                                                                                                                                                                                                  A;Gene: ox40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 1-256 «KWO»
A,Cross-references: UNIPROT:P20334; GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122
R;Koos S. S.; Kozak. C.A.; Kim, K.K.; Pickard, R.T.
J. Immunol. 152, 2256-2262, 1994
A,Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cross-references: UNIPROT:P47741; EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g3128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Milternate names: OX40 antigen
Milternate names: OX40 antigen
Milternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 148700; 148334; S34377
M;Calderhead, D.M.; Buhlmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
A;Reference number: 148700
A;Reture: translated from GB/EMBL/DDBJ
A;Accession: 148700
A;Molecule type: mRNA
A;Residues: 1-272 cRES>
A;Cross-references: UNIPROT:P47741; EMBL:Z21674; NID:g312827; PIDN:CAA79772.1; PID:g3128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 HYPCQPGQRVESQGDIVFGFRCVACAMGTFS-AGRDGHCRLWTNCSQFGFLTMFPGNKTH 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 K-DCRPGQELTKQG-----CXTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAVCIP----EPLPTEQY----GH----LTVIFLVMAACIFFLTTVQLGLHIWQLR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78
                                                                                                                                                                                                                                                                               T-cell antigen 4-1BB precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: B32393; 148879
R;Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. US.A. 86, 1963-1967, 1989
A;Title: cDNA sequence of two inducible T-cell genes.
A;Reference number: A32393; MUID:89184547; PMID:2784565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: U02567; NID: 91117783; PIDN: AAA93113.1; PID: 9409178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 SVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCP---KERCICVTPEYHCGDPQCKICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 15.6%; Score 203.5; DB 2; Length 256; Local Similarity 29.8%; Pred. No. 9e-10; nes 64; Conservative 26; Mismatches 84; Indels 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ajintrons: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: transmembrane protein
F;1-31/Domain: aginal sequence #status predicted <SIG>F;24-256/Product: 4-1BB protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: I48879; MUID: 94179805; PMID: 8133039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: :||| : ||| | RKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEG 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: 148879
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                         1 :||||| |
242 SCRFPEEEG 251
                                                             205 SFOFPEEERG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-256 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: B32393
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Matches
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C; Superfamily: mouse low-density lipoprotein receptor-related protein; LDL receptor ligar F;337-372/Domain: LDL receptor ligand-binding repeat homology sLDL1>
F;337-372/Domain: LDL receptor ligand-binding repeat homology sLDL2>
F;474-408/Domain: LDL receptor ligand-binding repeat homology sLDL2>
F;474-408/Domain: LDL receptor ligand-binding repeat homology sLDL2>
F;47-482/Domain: LDL receptor ligand-binding repeat homology sLDL4>
F;648-682/Domain: LDL receptor ligand-binding repeat homology sLDL5>
F;68-720/Domain: LDL receptor ligand-binding repeat homology sLDL5>
F;68-720/Domain: LDL receptor ligand-binding repeat homology sLDL5>
F;869-1097/Domain: LDL receptor ligand-binding repeat homology sLDL5>
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C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C; Accession: JE0315
R; Tomita, Y.; Kim, D.; Magoori, K.; Fujino, T.; Yamamoto, T.T.
J; Biochem. 124, 784-789, 1998
J; Biochem. 124, 784-789, 1998
A; Title: A novel low-density lipoprotein receptor-related protein with type II membrane IA; Reference number: JE0315; MUID: 98429596; PMID: 9756624
A;Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignment of A;Reference number: 137552; MUID:94170844; PMID:7510240
A;Status: 137552
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1.277 **REES>
A;Cross-references: UNIPROT:P43489; EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:g47295; C;Superfamily: CD27 antigen; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----GFRCVACAMGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 SYKPGVDCAPCPPGHPSPGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRDPPATQ-- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 ONTVCR--PCGPGFYNDVVSSKPCKPCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 LYAPGKEDCPKERCICVTPEYHC-GDPQCK----IC--KHYPCQPGQRVESQGDIVFG
                                                                                                                                                                                                                                                                                                                                                                                                                                        13 LCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERCICVTPEYHCGDP
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A;Status: preliminary
A;Status: mRNA
A;Medidues: 1-1113 <TOM*
A;Cross-references: UNIPROT:Q92319; DDBJ:AB013874; NID:g3869144;
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                                                                                                                                                                                                                                                                                                      / Match 9.4%; Score 122; DB 2; Length 277; Local Similarity 21.1%; Pred. No. 0.0057; nes 54; Conservative 22; Mismatches 80; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 LILLGEGESTVT----GLHCVGDTYPSNDRCCHECRPGNGMVSR----
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C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 137552
R;Latza, U; Durkop, H; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat
Bur. J. Immunol. 24, 677-683, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Mcererice number 12000; Mcererice number 12000; Mcererice number 1200 cdRA Macedon: A49053
A; Molecule type: mRNA
A; Mesiduces: 1-250 cdRA
A; Mesiduces: 1-250 cdRA
A; Cross-references: UNIPROT: P41272
A; Note: sequence extracted from NCBI backbone (NCBIN:128168, NCBIP:128169)
A; Note: sequence extracted from NCBI backbone (NCBIN:128168, NCBIP:128169)
A; Note: sequence extracted from NCBI receptor repeat homology
C; Superfamily: CD27 antigen, #status predicted <8IG>
E; 21-250, Product: CD27 antigen #status predicted <8IG>
F; 21-250, Product: CD27 antigen #status predicted <8IG>
F; 21-250, Product: CD27 antigen #status predicted <8IG>
F; 21-250, Product: NGF receptor repeat homology <NG3>
F; 21-250, Product: norpara homology <NG3>
F; 21-179/Region: proline/serine/threonine-rich
F; 11-179/Region: proline/serine/threonine-rich
F; 121-179/Region: transmembrane #status predicted <IMN>
F; 250, Domain: intracellular #status predicted <IMN>
F; 101-250, Domain: intracellular #status predicted <INT>
F; 102-250, Domain: intracellular #status predicted <INT>
F; 102-250, Domain: intracellular #status predicted <INT>
F; 102-250, Domain: intracellular #status predicted <INT>
F; 103-250, Domain: intracellular #status predicted <
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A;Title: Cloning and expression of murine CD27: comparison with 4-1BB, another lymphocyth, A;Reference number: A49053; MUID:93209296; PMID:8384562
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                                                                                                                          ---PLPTEQYGHLTVIFLVMAACIFFLTTVQLG 174
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                        CD27 antigen precursor - mouse
N;Alternate names: CD27L receptor; T cell activation antigen CD27
S;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Dec-1993 #sequence_revision 22-Apr-1995 #text_change 09-Jul-2004
C;Accession: A49053
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                                                                                                                                                                                                                                                                175 LHIWQLRRQHMCPRETQPFAEVQLSAEDAC---SFQFPEEERGEQTE 218
                                                                                                                                                                                                                                                                                                   Indels
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20.8%; Pred. No. 0.0027;
tive 30; Mismatches 93
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A;Residues: 1-459 <RES>
A;Cross-references: UNIFOT:062327; EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:943383
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
F;151-188/Domain: NGF receptor repeat homology <NGF>
                    R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P. Genomics 16, 214-218, 1993
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequenc A;Recession: 154182; MUID:93252381; PMID:8486360
A;Accession: 154182
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Apolecule type: mRNAA,
                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:1230195; OMIM:600979
A; Map position: 12p13.3-12p13.1
C; Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P36941; GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 CSRIRDIVCAI----CAENSYNEHWNYLIICQLCRPCDPVMGLEEIAPCTSKRKTÖCRCQ 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----CKH----YPCQPGQRVESQGDIVFG-FRCVACAMGTF--SAGRDGHCRL 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 WINCSOFGFLIMFPGNKTHNAVCIP--EPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLH 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 HTRCENQGLVEAAPGTAQSDTTCKNPLEPLPPEMSGTM-LMLAVLLPLAFFLLLATVFSC 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 DTVCADCEASMYTQVWNQFRTCLSCSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGDPQCKICKHY-PCQPGQRVES----QGDIVFGFRCVACAMGTFS--AGRDGHCRLWTN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: I48854
R;Powell, B.B.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: I48854; MUID:95178848; PMID:7873884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 AWGPLV-LGLFGLLAASOPOAVPPYASENQTCRDQEKEYYEPOHRICCSRCPPGTYVSAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----RCCSLYAPGKED-----CPKER---CICVTPEY---H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.8%; Score 115; DB 2; Length 435; Best Local Similarity 22.2%; Pred. No. 0.033; Matches 54; Conservative 23; Mismatches 94; Indels
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A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 CPKER-CICVTPEYHCG----
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Matches 54, Conserv
                                                                                                                                                                                                                                                             A; Residues: 1-435 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 IWK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: I48854
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A; Residues: 1-277 <STA.
A; Cross-references: UNIPROT: P25942; EMBL: X60592; NID: G29850; PIDN: CAA43045.1; PID: G29851
A; Cross-references: UNIPROT: P25942; EMBL: X60592; NID: G29850; PIDN: CAA43045.1; PID: G29851
B; Braesch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A; Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
A; Reference number: A60771; MUID: 89093941; PMID: 2463309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Map position: 20q12-20q13.2
Superfamily: CD27 antigen; NGF receptor repeat homology
Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: S04460; A60771
C;Accession: 1: Clark, E.A.; Seed, B.
EMBO J. 8, 1403-1410, 1989
A;Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor A;Reference number: S04460; MUID:89356608; PMID:2475341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
499 SSCVESCAGSSLCDSDSSL---SNCSQCEPITLELCMNLLYNHTHYPNYLGHRTQKEASI 555
                                                                 -----PEPLPTEQYGHLTVIFLVMAACIFFL--TTVQLGLHI--WQLRRQHMCPRETQ 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 -----ICVTPE-YHCGDPQCKIC-KHYPCQPGQRVESQGDIVFGFRCVACAMGTFS- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 KGTSETDTICTCEEGWHCTSEACESCVLHRSCSPGFGVKQIATGVSDTICEPCPVGFFSN 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 -AGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154 VSSAFEKCHPWTSCETKDLVVQQAGTNKTDVVCGPQ----DRLRALVVIPIIF-GILFAI 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 TTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQT----EEKCH 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-20/Domain: signal sequence #status predicted <SIG>
21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
21-193/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor necrosis factor receptor 2-related protein - human
C;Species: Homo sapiens (man)
£;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
                                                                                                                         556 SWESSLFPALVQINCYK----YLMFFACTILVPKCDVNTGQRIPPCRLLCEHSKERCES
                                                                                                                                                                                                                                                                611 VLGIVGLQWPEDTDCNÓFPEESSDNÓTCLLPNEDVEECSPSHFKCRSGRCVLGSŘ 665
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F;216-277/Domain: intracellular #status predicted <CYT>
F;153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                              192 PFAEVQLS-AEDACSFQFPEERGEQT-----EE-----KCHLGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
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                                                                                                                                                                                                                                                                                                                                                                                                        A60771
B-cell activation protein CD40 precursor - human
N;Alternate names: B-cell surface antigen Bp50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-references: GDB:215268; OMIM:109535
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Best Local S:
Matches 50
                                                                 143
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72;

42 57 68

---CGPGKVQNGSGNNT-

Length 459;

Indels

63; DB 2;

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Daccession: A35356; A36476; A36007; A23666; B35010; I38094
C;Accession: A35356; A36475; A46416; A36007; A23666; B35010; I38094
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K. Science 248, I019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and NA;Reference number: A35356; MUID:90260639; PMID:2160731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Residues: 1-195, R', 197-461 <KOH>
A.Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R.Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; NJ
Mineral Differential increase of an alternatively polyadenylated mRNA species of murine A,Reference number: A46476, MUID:92105763; PMID:1370315
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A,Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-305 < TORS.
A; Residues: 1-305 < TORS.
A; Cross-references: UNIPROT: P27512; GB: M83312; NID: G1553058
A; Note: sequence extracted from NCBI backbone (NCBIN: 75206, NCBIP: 75207)
A; Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
B; Grimmldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992
A; Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A; Reference number: A46515; MUID: 93094586; PMID: 1281194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 TABSDIVCTCKEGGHCTSKDCEACAQHTPCIPGFGVMEMATETIDIVCHPCPVGFFSNQS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 DLCQPGSRLTSHCTALEKTQCHPCDSGBFSAQMNREIRCHQHRHCE---PNQGLRVKKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 DLGQP-----SVVEEPGCGP---GKVQNGSGNNTRC-----CSLYAPG-----KED
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N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-287,'LV' <GRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: BALB/C, liver
A;Note: sequence extracted from NCBI backbone (NCBIP:120357)
C;Comment: For an alternation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Comment: For an alternative splice form, see PIR:A46515.
C;Comment: For an alternative splice form, see PIR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;105-144/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.0%; Score 104.5; DE Best Local Similarity 25.2%; Pred. No. 0.18; Matches 38; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GRDGHCRLWTNCSQFGFLTMFPGNKTHNAVC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 SLFEKCYPWISCEDKNLEVLQKGISQINVIC 186
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A35356
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A;Residues: 1-474 <LEW3-
A;Residues: 1-474 <LEW3-
A;Cross-references: UNIPROT: P25119; GB:M60469; NID:9199827; PIDN:AAA39752.1; PID:9199828
R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular caloning and expression of the type 1 and type 2 murine receptors for
A;Reference number: A40254; MUID:91246168; PMID:1645445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     icross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044; Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homologiseywords: cytokine receptor; transmembrane protein

7.1-22/Domain: signal sequence #status predicted ASIG>
7.47/Domain: signal sequence #factor receptor type 2 #status predicted AMT>
7.40-77/Domain: NGF receptor repeat homology ANG1>
7.9-120/Domain: NGF receptor repeat homology ANG2>
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                                                                                                                                                                                                                                                                                                                                                                   C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: B38634; A40254; $54816
C;Accession: B38634; A40254; $54816
F;Lewis, M.; Tartaglla, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, F.Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of CDNAs for two distinct murine tumor necrosis factor A;Reference number: A38634; MUID:91187885; PMID:1849278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828 R;Kissonerghis, M.; Fellowes, R.; Feldmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995 A;Description: Characterization of the promoter region of the murine p75-TNF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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118 SG--SCROCMRLSKCGPGFGVASSRAPNGNVL----CKACAPGTFSDTTSSTDVCRPHRI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 WATCHTVPAOVVLTPYKP----EPGYECQISOEYYDRKAQMCCAKCPPGQYVKHFCNKTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGDPQCKICKHY-PCQPGQRVES----QGDIVFGFRCVACAMGTFS--AGRDGHCRLWTN
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                                                                                                                                                                                                                                                                                                            tumor necrosis factor receptor type 2 precursor - mouse C;Species: Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSOFGFLTMFPGNKTHNAVCIPEPLPT 148
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                                                                                                                     A;Reference number: S54816
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les 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-474 <GOO>
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A:Reference number: A48416: MUID:91370690: PMID:1966549	Db 176 TDICRPHOICNVVAIPGNASMDAVCTSTSPTRSMAPGAVHLPQPVST 222
A; Accession: A48416	158 BINMAACTERITUOLGIHIMOIBROHMCPRETOPPARVOLSARDACSFOPP 209
A; Mocule type: mRNA; protein A: Posidine: 23.461 / DRMA.	223
A;Crose_truces: 23-401 CDMN: A;Crose_truces: 25-401 CDMN: A;Crose_truces: 25-61368; NID:g235648; PIDN:AAB19824.1; PID:g235649 A;Crose_truces: 24-1-36-1-36-1-36-1-36-1-36-1-36-1-36-1-3	1700
R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.	RESULT 14
y DNS. 11. 0131 0131 0131, 1330, 1330, 1330 or tumor necrosis factor and demonstral or control of a receptor for tumor necrosis factor and demonstral necessary.	protein-tyrosine kinase (EC 2.7.1.112) neu precursor - rat C. Gandise. Dattus norvening (Norway rat)
•	C.)Diction
	R;Bargmann, C.I.; Hung, M.C.; Weinberg, R.A.
;	Nature 319, 226-230, 1986 A; Title: The neu oncogene encodes an epidermal growth factor receptor-related protein.
; Brockhaus, M.	A;Reference number: A24562; MUID:86118662; PMID:3945311 A;Accession: A24562
stinct tumor ned	A;Molecule type: mRNA A;Residues: 1-1260 <bar></bar>
	A;Cross-references: UNIPROT:P06494; EMBL:X03362; NID:956745; PIDN:CAA27059.1; PID:956746 R;Masui, T.; Mann, A.M.; Macatee, T.L.; Garland, E.M.; Okamura, T.; Smith, R.A.; Cohen, E
pe: protein 3-40.65-69:136-141:300-306 <1.08>	Carcinogenesis 12, 1975-1978, 1991 A:Title: Direct DNA sequencing of the rat neu oncogene transmembrane domain reveals no m
	2-thiazolyl]formamide or N-methyl-N-nitrosourea. A:Reference number: A61204: MUID:92035293: PMID:1682063
oteins purified from human urine. Evidence	A;Accession: Adizo4
00100177	A; Octains: president and president to the control of the control
	A; Residues: 63/-663, 'V', 665-702 < MAS> A; Note: authors translated the codon GCA for residue 25 as Val
A;Residues: 27-31 <eng> R;Kuhnert, P.: Kemper, O.: Wallach, D.</eng>	C;Genetics: A;Gene: neu
	C; Superfamily: epidermal growth factor receptor; protein kinase homology
ng and partial functional characterization of the 5' region of ; MUID:95121934; PMID:7821811	C; Keywords: Air; autophosphoryiation; auplication; giycopiotein; phosphoriation; phosphoriati
Accession: 138094 Status: preliminary; translated from GB/EMBL/DDBJ	F;20-1250//Froduct: procentry/Osine Ainase Heu #scarus predicted Aina; F;658-680/Domain: transmembrane #status predicted AINN>
	F;723-988/Domain: protein kinase homology <kin> F;731-739/Region: protein kinase ATP-binding motif</kin>
324.1; PID:g825701	F;71,191,263,535,576,634/Binding site: carbohydrate (Asn) (covalent) #status predicted F;691/Binding site: phosphate (Thr) (covalent) #status predicted
	P;758/Active_site: Lys #status predicted F:882.1227.1253/Binding site: phosphate (Tvr) (covalent) #status predicted
	Onexy March 7 9% Score 102 5: DR 1: Length 1260:
A/introms: 20/3 A/introms: 20/3 A/shote: The list of introms is incomplete A.conomistrally: Annowable factor accounts the commentary to th	92; 87: Ta: Indels
rks); wer receptor repeat mbrane protein	וים כיבסייי ויי היים אים אים פוסייים אין אים האים אים פוסייים אין היים אים אים אים אים אים אים אים אים אים
F:1-22/Jomain: Signal Sequence #Status predicted <510-5 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <mat></mat>	
F:78-119/Domain: NGF receptor repeat nomology <ng2></ng2>	OZI GEGETTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
F;120-162/Domain: NGF receptor repeat homology <ng3> F;164-201/Domain: NGF receptor repeat homology <ng4></ng4></ng3>	88 VESQGDIVYGFKCVACAMGIFSAGKDGHCKLMINUSQFGFLIMFFG
	5/5 - UNSSETTERGSEADQCAACAHIKDSSSCVARCESGVARDDSIMFIMAFFDEEGACQFCF1
F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted	Qy 134 NKTHNAVCIPE-PLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQLRRQ 183
atch 7.9%; Score 102.5; DB cal Similarity 22.4%; Pred. No. 0.38;	Db 634 NCTHSCVDLDERGCPAEQRASPVTFIİATVEGVLLFLILVVVVĞILİ-KRRRQ 685
nes 52; Conservative 18; Mismatc	RESULT 15
Qy 29 CGPGKVQNGSGNNTRC	A53102 alpha-2-macroglobulin receptor precursor - chicken NyAlternate names: CD91, LDL receptor-related protein 1, low density lipoprotein recepton
Qy 60 -CICVTPEYHCGDPQCKICKHY-PCOPGQRVESQGDIVEGFRCVACAMGTFSAGR 112	C;Species: Gallus gallus (chicken) C;Date: 04-509=1998 #Beequence_revision 04-Sep-1998 #text_change 09-Jul-2004
Db 117 ICTC-RPGWYCALSKQEGCRLCAPLRKCRPGFGVARPGTETSDVVCKPCAPGTFSNTTSS 175	
Qy 113 DGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVI 157	A;Title: The somatic cell-specific low density lipoprotein receptor-related protein of th A;Reference number: A53102; MUID:94103212; PMID:7506255

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Search completed: October 26, 2005, 15:52:33
Job time : 27.307 secs
                                                                                                                                                                                                                                                                                                     F,3533-3567/Domain: L
F,3572-3606/Domain: L
F,3610-3644/Domain: L
F,3651-3687/Domain: L
F,3692-3728/Domain: L
F,3738-3774/Domain: L
                                                                                                                                                                                              F;3331-336(Domain: I
F;3371-346(Domain: I
F;3450-3448(Domain: I
F;3450-3486(Domain: I
F;3491-3528(Domain: I
                          F;2983-3018/Domain: E;3026-3065/Domain: E;3026-310/Domain: E;3111-3153/Domain: E;3154-3197/Domain: E
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F;3943-4420/Domain:
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                                                                                                                                      3198-3238/Domain:
                                                                                                                                                          F;3239-3281/Domain:
F;3291-3327/Domain:
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                                                                                                  Gisperfamily: alpha-2-macroglobulin receptor; EGP homology; LDL receptor ligand-binding cisperfamily: alpha-2-macroglobulin receptor; EGF homology; LDL receptor ligand sequence flattus predicted <EIG.
File-1942/Domain: alpha-2-macroglobulin receptor SISK chain flattus predicted <EISK.
File-1942/Domain: alpha-2-macroglobulin receptor flattus predicted <EISK.
File-1942/Domain: DLR receptor ligand-binding repeat homology <LDL2->
File-1942/Domain: DLR receptor ligand-binding repeat homology <LDL2->
File-1940/Domain: DLR receptor ligand-binding repeat homology <LDL2->
File-1940/Domain: DLR receptor WIPD-containing repeat homology <WAND2->
File-1940/Domain: DLR receptor WIPD-containing repeat homology <WAND3->
File-1940/Domain: DLR receptor ligand-binding repeat homology <WAND3->
File-1940/Domain: DLR receptor ligand-binding repeat homology <WAND3->
File-11940/Domain: DLR receptor ligand
             ;Molecule type: mRNA
;Residues: 1-4543 <NIM>
:Cross-references: UNIPROT:P98157; GB:X74904; NID:g438006; PIDN:CAA52870.1; PID:g438007
;Complex: The alpha-2-macroglobulin receptor complex consists of noncovalently-associat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <YW30><YW31></YW32></YW33>
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2816-2851/Domain:
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F;4444-4543/Domain: intracellular #status predicted <INT>
F;116,138,187,276,359,448,731,926,1048,1152,1153,1193,1216,1305,1509,1556,1573,1614,1643,
F;116,138,1387,3952,4074,4124,4178,4178/Binding site carbohydrate (Asn) (covalent)
F;168,2995/Modified site: erythro-beta-hydroxyasparagine (Asp) #status predicted
F;2955/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted
tin: LDL receptor ligand-binding repeat homology <LDLJS>
tin: LDL receptor ligand-binding repeat homology <LDLJS>
tin: EGF homology <EG11>
tin: LDL receptor WTD-containing repeat homology <WW35>
tin: LDL receptor WTD-containing repeat homology <WW37>
tin: LDL receptor WTD-containing repeat homology <WW39>
tin: LDL receptor WTD-containing repeat homology <WW39>
tin: LDL receptor WTD-containing repeat homology <WW39>
tin: LDL receptor Ilgand-binding repeat homology <LDLDN>
tin: LDL receptor ligand-binding repeat homology <LDLN>
tin: LDL receptor WTD-containing repeat homology <WW41>
tin: LDL receptor WTD-containing repeat homology <WW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----PEYHCGDPQCKICKHYPCQPGQRVESQGDIVF---GFRCVA---- 102
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Best Local Similarity 28.0%
Matches 47; Conservative
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THE PACE OLAWN (USPID)

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035714 mus musculu 0964k3 mus musculu 0995u5 homo sapien 00711 homo sapien 02034 mus musculu 080037 mus musculu 0800m9 mus musculu 071£55 mus musculu 071£55 mus musculu 075av8 felis silve 0761D paralichty 060112 mus musculu 08012 mus musculu 008712 mus musculu 00877 mus musculu 00877 mus musculu 00873 mus musculu 00264 oryctolagus 080315 mus musculu 00520 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 035305 mus musculu 0996q6 homo sapien 078305 ovis aries 080mq2 ovis aries
                                                              October 26, 2005, 15:29:08 ; Search time 112.299 Seconds (without alignments) 1039.676 Million cell updates/sec
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                                                                                                              US-09-545-998B-2
1301
1 MGAWAMLYGVSMLCVLDLGQ......PEEERGEQTEEKCHLGGRWP 228
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                              1612378 seqs, 512079187 residues
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TR18 HUMAN
TNR9 HUMAN
TNR9 MOUSE
Q8R037
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T118 MOUSE
T118 MOUSE
00276 MOUSE
T118 RAT
T118 RAT
T111 MOUSE
TR11 MOUSE
TNR7 MOUSE
TR11 MOUSE
TNR7 HUMAN
T118 BOVIN
TNR5 BOVIN
TNR5 BOVIN
TNR3 MOUSE
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CORI_MOUSE
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Listing first 45 summaries
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Q71F55
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Q75SV8
Q76LB4
Q6PI12
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Match Length
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Perfect score:
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                                            OM protein
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٠.	Q7zzy5	Q7ZZY5	N	186	8.3	108.5	~
	Q8k3£9	Q8K3F9	7	1259	8.5	110.5	ч
rattus	080wy6	TR1B_RAT	ч	474	8.5	110.5	0
rattus	Q6vau8	Q6VAÜ8	~	461	8.5	110.5	σ
	095407	TR6B_HUMAN	н	300	8.5	110.5	8
	O9nxf8	ZDH7_HUMAN	н	308	8.8	114	7
homo	P36941	TNR3_HUMAN	-	435	8.8	115	9
salve	09nd60	OSD460	N	302	6.8	115.5	ß
	Q86yk5	Q86YKS	~	223	8.9	115.5	4
• •	Q6gln3	OGGLN3	N	387	9.1	118.5	m
	P25942	TNRS_HUMAN	ч	277	9.1	118.5	~

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ALIGNMENTS

SULT 1 18 MOUSE STANDARD; 035144, 09JKR1; 09JKR2; 09J 16-CCT-2001 (Rel. 40, Creat				RP SEQUENCE FROM N.A. (ISOFORM A). RC STRAIN-BALB/c; RX MEDLINE-20256302; PubMed=10798444; DOI=10.1089/104454900314474; RX MCDENIAIN G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A., RA Delfino D., Migliorati G., Riccardi C.; RT "Gene structure and chromosomal assignment of mouse GITR, a member of RT the tumor necrosis factor/nerve growth factor receptor family.";		RD 141 RC STRAIN=C57BL/6J; TISSUE=Thymus; RX MEDLINE=223546813; PubMed=1246681; DOI=10.1038/nature01266; RX MEDLINE=223546813; PubMed=1246681; DOI=10.1038/nature01266; RA MEDLINE=223546813; PubMed=1246681; DOI=10.1038/nature01266; RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., RA Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.B., Cousins S., RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
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RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Radott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

RA Ravasi T., Reed J.C., Reed D.J., Rang B.Z., Ringwald M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sultana R., Takkenaka Y., Taylor M.S., Tesadala R.D., Tomita M.,

RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watunabe Y., Walls C.,

RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carminci P., Hayatsu N.,

RA Hara A., Hashizume W., Imoteni R., Ishii Y., Itoh M., Kagawa I.,

RA Hara A., Hashizume W., Imoteni K., Ishii Y., Itoh M., Kagawa I.,

Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,

Raunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Mara R., Hayashizaki Y.,

RA Hara R., Rayashizaki Y.,

Ranalysis of the mouse transcriptome based on functional annotation of

RA NAMARIAN. B. M. Wall R. M. M. Rayaraki M. Rayaraki M. Rayaraki M. Rayaraki M. Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Rayaraki M., Ra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity).
SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and TRAF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (By similarity).
SUBCELULIAR LOCATION: Type I membrane protein (isoforms A, B and C); secreted (isoform D).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- INDUCTION: Up-regulated in peripherical mononuclear cells after antigen stimulation/lymphocyte activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Receptor for TNFSF18. Seems to be involved in interactions between activated T lymphocytes and endothelial and in the regulation of T cell receptor-mediated cell death. Mediated NF-kappa-B activation via the TRAF2/NIK pathway (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, U82534; AAB81243.1; -.

REMBL, AF229432; AAF61566.1; -.

REMBL, AF229433; AAF61566.1; -.

REMBL, AF229433; AAF61566.1; -.

REMBL, AF229434; AAF61568.1; -.

REMBL, AF229434; AAF61568.1; -.

REMBL, AF229434; AAF61568.1; -.

REMBL, AF229434; AAF61568.1; -.

REMBL, AF229434; AAF6156.1; -.

REMBL, AF229432; AAFF AFE NGF

REMBL, AF229432; ARFR NGFR 2; FALSE NGG.

REMBL, AF129433; AAF615194; Glycoprotein; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isold=035714-4; Sequence=VSP 006509;
TISSUE SPECIFICITY: Preferentially expressed in activated T
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Potential.
Cytoplasmic (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=035714-3; Sequence=VSP_006511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=035714-2; Sequence=VSP_006510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=035714-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Potential,
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                                                                                                                                                                                                                                                      N-linked (GlcNAc. .) (Potential).
NCSQPGFLTWFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVM
AACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAED
ACSFQFPEEERGEQTEEKCHLGGRWP -> KDPAIRGGAVV
                                                                                                                                                                                                                                                                                                                                                                                                                      -> VLLQRPSHSRRCSCQLRMLAASSSLRRNAGSRQKKSVI
WGVGGHEAWSSSVPQARRYKTCPAIPLVRAGAMLCTLPWAW
PCSPQQWRKWVYSSGELRLGPMAAFLI (in isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOLCPREGENVSQAPHLPQFYYRDPAIRGGAVVS (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VSP_006510.
ETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 icviperhcdopockickHypcopGokvesgGDIvPGFRCVACAMGTFSAGRDGHCRLWT
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                                                                                                                                                                                                                                                                                                                                                                                                ETQPFAEVQLSAEDACSFQFPEEBRGEQTEEKCHLGGRWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
TNFR-Cys 1.

TNFR-Cys 2.

TNFR-Cys 2.

By similarity.

By similarity.

By similarity.

By similarity.

By similarity.

N-linked (GlCNAc. ..) (Potential).

N-linked (GlCNAc. ..) (Potential).

N-linked (GlCNAc. ..) (Potential).
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched
library, olone:C130084C11 product:tumor necrosis factor receptor superfamily, member 18, full insert sequence.
Name=Infrsf19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
0
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
Anyashida S., Furuno M., Hanaqaki T., Hara A., Hashizume W.,
Anyashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
An Hori F., Imotani K., Ishii Y., Itoh M., Kaqawa I., Kauukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Sasaki D., Shibata K., Shinaqawa A., Shiraki T., Sogabe Y., Taqami M.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
B EMBL, AKOBSTO: T. Takawa A., Muramatsu M., Hayashizaki Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6J; TISSUB=Head; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                            οŧ
                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Ttoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sunibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakmura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kabhiwagi K., Fujiwake S., Inoue K., Tozawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                             "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.5%; Score 1294; DB 2; Length 250; 100.0%; Pred. No. 2.4e-105; ive 0; Mismatches 0; Indels (
                        STRAIN=CS7BL/61; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 AA; 27814 MW; 6963E94F414C16B4 CRC64;
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GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR006210; IEGF.
InterPro; IPR001368; TNFR_C6.
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STRAIN=C57BL/6J; TISSUE=Head;
The FANTOM CONSOITIUM,
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SMART; SM00208; TNFR; 2.
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Best Local Similarity
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SEQUENCE FROM N.A.
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61 ICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT 120
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MEDLINE=99175482; PubMed=10074428; DOI=10.1016/S0960-9822(99)80093-1;
MEDLINE=99175482; PubMed=10074428; DOI=10.1016/S0960-9822(99)80093-1;
Gurney A.L., Mareters S.A., Huang R.M., Pitti R.M., Mark D.T.,
Baldwin D.T., Gray A.M., Dowd A.D., Brush A.D., Heldens A.D.,
Schow A.D., Goddard A.D., Wood W.I., Baker K.P., Godowski P.J.,
                                             121 NCSOFGFLTMFPGNKTHNAVCIPEDLPTEQYGHLTVIFLVMAACIPFLTTVQLGLHIWQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE=99156876; PubMed=10037686; DOI=10.1074/jbc.274.10.6056; Kwon B., Yu K.-Y., Ni J., Yu G.-L., Jang I.-K., Kim Y.-J., King L., Liu D., Wang S.-X., Kwon B.S.; "Identification of a novel activation-inducible protein of the tumor necrosis factor receptor superfamily and its ligand."; J. Biol. Chem. 274:6056-6061(1999).
                                                                                                                                                                                                                                                                                      TRIB HUMAN STANDARD; PRT; 241 AA.

Q9Y5U5; O95851; Q9NYJ9;
16-OCT-2001 (Rel. 40, Created)
15-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Tumor necrosis factor receptor superfamily member 18 precursor (Glucocorticoid-induced TNFR-related protein) (Activation-inducible TNFR family receptor) (UNQ319/PRO364).
Name=TNFRSF18; Synonyms=AITR, GITR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ashkenazi A.; "Identification of a new member of the tumor necrosis factor family and its receptor, a human ortholog of mouse GITR."; Curr. Biol. 9:215-218(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                  181 RRQHMCPRETQPFAEVQLSAEDACSFQFPEEERGEQTEEKCHLGGRW 227
                                                                                                                                                         Cell Death Differ. 7:408-410(2000).
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Genome Res. 13:2265-2270(2003).
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1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC 1 MGAWAMLYGVSWLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERC

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61 ICVTPEYHCGDDQCKICKHYPCQPGQVVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWT

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TNR9 HUMAN
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TNFR-Cys 3.

By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAc. . .) (Potential).
TOFGFLTVPFGNKTHINQUESCOMMPRETQLILEVDAR.
CVLLLTSAQLGLHIWQLRSQCMMPRETQLILEVPESTEDAR.
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AASSPRKSGASDRQRREGGWETCOEPGRPPOEPTAASPSP
GAPQAAGALRSALGRALLPWQCKWVQEGGSDQRPGPCSSAA
AAGPCRRERETQSWPPSSLAGPDGVGS (in isoform
                                                                                                                                                                                  cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=2; Synonyms=GITR*-D; 100508; 1soft=2; Synonyms=GITR*-D; 1soft=2; Sequence=VSP 006508; 1SSUB SPECIFICITY: Expressed in lymph node, peripheral blood leukocytes and weakly in spleen.
INDUCTION: Up-regulated in peripherical mononuclear cells after inDuction: Up-regulated in peripherical mononuclear cells after antigen stimulation/lymphocyte activation.
INDUCATION: Contains 3 TNFR-Cys repeats.
PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
Signal peptide prediction based on analysis of experimentally verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
-! FUNCTION: Receptor for TWRSF18. Seems to be involved in interactions between activated T lymphocytes and endothelial and in the regulation of T cell receptor-mediated cell death.
Mediated NF-kappa-B activation via the TRAFZ/NIK pampay.
                                                                                                                                                                                                                                                                    SUBUNIT: Binds to TRAFI, TRAF2, and TRAF3, but not TRAF5 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM; 603905; ...
GO; GO: 0005031; F: tumor necrosis factor receptor activity; TAS.
GO; GO: 0005016; P: anti-apoptosis; TAS.
GO; GO: 0007165; P: signal transduction; TAS.
InterPro; IPR001368; TNPR. GG.
PROSITE; PSO0652; TNFR NGFR. 1; FALSE NGG.
PROSITE; PSO0650; TNFR NGFR. 2; FALSE NGG.
Alternative splicing; Direct protein sequencing; Glycoprotein;
Receptor; Repeat; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
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SQCMWPRE -> K (in Ref. 2).
90DC3B4AA7E82CBE CRC64;
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TNFR-Cys 1.
                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=2;
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ALTERNATIVE PRODUCTS:
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241 AA;
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Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.,
NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
of Genome Sciences, Seattle, WA (WEL: http://egp.gs.washington.edu).";
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                   54 DCPKERCICVTPEYHCGDPQCKICKHYPCQPGQRVESQGDIVFGFRCVACAMGTFSAGRD
                                                                                                                                                                                                                                                                                       66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE
                                                                                                                           1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRCCSLYA-----PGKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA)
                                                           Gaps
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MEDLINE=94085794; PubMed=8262389; DOI=10.1016/0378-1119(93)90110-0;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Kwon B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND VARIANTS THR-56; ASN-115 AND ASP-176.
   Length 241;
                                                           Indels
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                                                               61;
   DB 1;
56.5%; Score 735.5; DB 1
57.0%; Pred. No. 1.9e-56;
tive 31; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Immunol. 24:2219-2227(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=TNFRSF9; Synonyms=CD137, ILA;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94374434; PubMed=8088337;
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                             Best Local Similarity 57.09
Matches 134; Conservative
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Woffwan N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broaks S.A., McDwan D.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Altohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Altalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Altohards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
All Month and initial analysis of more than 15,000 full-length human
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A Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
Jang I.-K., Lee Z.-H., Kim H.-H., Hill J.M., Kim J.-D., Kwon B.S.;
T anovel leucine-rich repeat protein (LRR-1): potential involvement in 4-1BB-mediated asgnal transduction.";
MOI. Cells 12:304-312(2001).
L. FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T cell activation.
C-1-FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T cell activation.
LRR-repeat protein JLRR-1.
C-1-SUBUNIT: Interacts with TRAF1, TRAF2 and TRAF3. Interacts with LRR-1.
C-1-SUBUNIT: LAR-1.
C-1-SUBURITY: Contains 4 TNFR-Cyg repeats.
C-1-SIMILARITY: Contains 4 TNFR-Cyg repeats.
C-1-DATABASE: NAME-PROW! NOTE-CD guide CDW137.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD28-independent, TRAF2-dependent costimulation of resting T cells by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arch R.H., Thompson C.B.; "4-1BB and Ox40 are members of a tumor necrosis factor (TNF)-nerve growth factor receptor subfamily that bind TNF receptor-associated factors and activate nuclear factor kappaB."; Mol. Cell. Biol. 18:558-565(1998).
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Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 24-38.

PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally verified cleavage sites.";
Protein Sci. 13:2819-2824(2004).
                                         Pearce A.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH LRR-REPEAT PROTEIN 1/LRR-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERACTIONS WITH TRAF1; TRAF2 AND TRAF3.
MEDLINE=98078711; PubMed=9418902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Exp. Med. 187:1849-1862(1998).
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[6]
SEQUENCE FROM N.A.
                                                                                                          FROM N.A.
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                                                                                                                                 TISSUE=Kidney
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105 MGTFSAGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPE------PLPTEQY 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 GHLTVIF-----LVMAACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAE-VQLS-AEDAC 204
  and for commercial
                  (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                      GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0005887; C:integral to plasma membrane; TAS.

BR GO; GO:0004917; P:induction of apoptosis; TAS.

BR GO; GO:0008285; P:inegative regulation of cell proliferation; TAS.

BR InterPro; IRR001368; TWRR_c6.

BR PEAM; PP000209; TWRR_c6; 2.

BR SWART; SM00208; TWRR, 2.

BR PROSITE; PS00652; TWRR_NGFR_1; 1.

RROSITE; PS00652; TWRR_NGFR_1; 1.

RROSITE; PS00650; TRRR_NGFR_1; 1.

REPEAM; Signal; Transmembrane.

T SIGNAL
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N-linked (GlCNAc. . .) (Potential).
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    k; Score 228.5; DB 1; Length 255;
    k; Pred. No. 5.2e-12;
    Mismatches 97; Indels 55.

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F3A563FE5EF00460 CRC64;
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TNFR-Cys 1.
TNFR-Cys 2.
TNFR-Cys 3.
TNFR-Cys 4.
Interaction with LRR-1.
By similarity.
By similarity.
By similarity.
By similarity.
    Usage
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                                                                        EMBL; U03397; AAA53133.1; -.
EMBL; L12964; AAA62478.2; -.
EMBL; AX438976; AR65440.1; -.
EMBL; AL009183; CA857398.1; -.
EMBL; BC006196; AAH06196.1; -.
PIR; I38426; I38426.
HSSP; Q92956; 1JWA.
Genew; HGNC:11924; TNPRSF9.
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3D-structure; Direct protein sequencing; Glycoprotein; Receptor;
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                         182 GHSPQIISFFLALTSTALLFLLFFLTLRFSVVKRGRKKLLYIFKQPFMRPVQTTQEEDGC 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell activation.
SUBUNIT: Principally an homodimer, but also found as a monomer.
Associates with p56-LCK. Interacts with TRAF1, TRAF2 and TRAF3 (By

similarity).
-1. SUBCELLULAR LOCATION: Type I membrane protein.
-1. TISSUB SPECIFICITY: Expressed on the surface of activated T cells.
-1. INDUCTION: Optimal by PMA and ionomycin.
-1. SIMILARITY: Contains 4 TNFR-Cys repeats.

                                                                                                                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last sequence update)
25-OCT-2004 (Rel. 17, Last annotation update)
Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).
Name=Tnfrsel; Synonyms=Cd137, Cd157, ILA, Ly63;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93139510; PubMed=7678621;
Pollok K.B., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! - FUNCTION: Receptor for TNFSF14/4-1BBL. Possibly active during T
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94179805; PubMed=8133039;
Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
"Genomic organization and chromosomal localization of the T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kwon B.S.;
"Inducible T cell antigen 4-1BB. Analysis of expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=89184547; PubMed=2784565;
Kwon B.S., Weisman S.M.;
"cDMs sequences of two inducible T-cell genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989)
                                                                                                                                                                                                                          256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00652; TNFR NGFR 1; 1.
PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION, AND SEQUENCE OF 24-29.
<del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDB; 1D0J; X-ray; G/H/I/J/K=230-236.
MGD; MGI:1101059; Thfrse9.
InterPro; IPR009030; Grow fac_recept.
InterPro; IPR001368; TNFR_G6.
                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunol. 152:2256-2262(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J04492; AAA40167.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U02567; AAA93113.1; -. PIR; B32393; B32393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00020; INFR c6; 1. SMART; SM00208; INFR; 2.
                                                                                                                                                                                                                          STANDARD;
                                                                  205 SFOFPEEERG 214
                                                                                                              242 SCRPPEEEEG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen 4-1BB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function.";
                                                                                                                                                                                                                        TNR9 MOUSE
P20334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Immunol.
                                                                                                                                                                                               TNR9 MOUSE
                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                 PATTE BERNANDER PRESENTATOR PRESENTATOR PRESENTATOR PROPERTY AND PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY PROPERTY P
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103 K-DCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWINCSLDGRSVLKTGTTEK 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 DVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLALIFITLLFSVLKWI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Uterus,
MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleron M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T. E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Perange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 SVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCP---KERCICVTPEYHCGDPQCKICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 SIGGOPNC-----NICRVCAGYFRFKKFCSSTHNAECECI-EGFHCLGPOCTRCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 HYPCQPGQRVESQGDIVFGFRCVACAMGIFS-AGRDGHCRLWINCSQFGFLIMFPGNKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84; Indels 41; Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                         Cycoplasmic (Potential).
TNRP-Cys 1.
TNRP-Cys 3.
TNRP-Cys 4.
By similarity.
                                                       Tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length
                                                                                      superfamily member 9.
Extracellular (Potential).
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 RQHMCPRETQPFAEVQLSA--EDACSFQFPEEERG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 KKKFPHIFKOPFKKTTGAAQEEDACSCRCPOEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.6%; Score 203.5; DB 1
29.8%; Pred. No. 8.1e-10;
tive 26; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     211 AA
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27598 MW;
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 :
256 AA;
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102 137

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SEQUENCE FROM N.A. STRAIN=C57BL/6; TISSUE=Thymus;
                                                                                                                                                                                                                                                                                                                                                                                                          67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 -DC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Tnfrsf14;
                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6MM080
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                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 SIGGQPNC-----NICRVCAGYFRFKKFCSSTHNAECECI-EGFHCLGPQCTRCE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 HYPCQPGQRVESQGDIVFGFRCVACAMGTFS-AGRDGHCRLWTNCSQFGFLTMFPGNKTH 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 NAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....SVTPEGGPAFKKTT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 SVVEEPGCGPGKVQNGSGNNTRCCSLYAPGKEDCP---KERCICVTPEYHCGDPQCKICK 78
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Blakesley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Green E.D., Grimman J.W., Green E.D., School B.C., Grimman and intial analysis of more than 15,000 full-length human and mouse CDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 K-DCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=TNFSF5;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tregaskes C.A.;
Thesis (2001), University of Reading, Reading, UNITED KINGDOM
EMBL; AJP93700; CAC20218.1; -.
HSSP; Q92956; LJMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 28.1%; Pred. No. 3.4e-08;
Matches 56; Conservative 20; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:11010.05.15.

MGD; MGI:1100.05615; C:extracellular space; TAS.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

InterPro; IPR001061; Antihaemostatic.

InterPro; IPR001368; TNFR C6.

Pfam; PF00020; TNFR C6; 1.

SMART; SM00208; TNFR; 2.

PROSITE; PS01186; EGF 2: UNKNOWN 1.

PROSITE; PS00652; TNFR NGFR 1; 1.

SEQUENCE 211 AA; 22452 MW; IBECA84EA32A8D50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO28507; AAH28507.1; -.
HSSP, Q92956; 1JMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO:0016020; C:membrane; IEA.
GO:0004888; F:transmembrane receptor activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       155 DVVCGP---PVVSFSPSTTI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 LSA--EDACSFOFPEERG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 GAAQEEDACSCRCPQEEEG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01 MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                          TISSUE=Uterus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             090002
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159 TEPCHFWTSCEEKGLVVKVKGTNTSDVIC----ESSRRSSLSVLIPITAAVV----TCL 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 MHCSDASCQTCVENEPCKQG------FGFVAAMAEARMTSPCEPCAEGTFSNVSSK 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 DGHCRLWINCSQFGFLIMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVWAACIFFLTTVQ 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 YHCGDDQCKIC-KHYPCQPGQRVESQGDIVFGF------RCVACAMGTFS--AGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGAWAMLYGVSMLCVLDLGQPSVVEEPGCG-PGKVQNGSG----NNTRCCSLYAPGKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 106;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor receptor superfamily member 14 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos G.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY264405; AAO89081.1; --
HSSP; Q92956; LJWA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.5%; Score 175; DB 2; Length 276; 23.5%; Pred. No. 2.8e-07; tive 34; Mismatches 78; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           173 LGLHIW-----QLRRQHMCPRETQPFAEVQLSAEDACSFQFPEBE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:2675333; Tnfrsf14.

MGD; GO:0016020; C:membrane; IEA.

GO; GO:00046915; P:transmembrane receptor activity; IEA.

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0007165; P:immune response; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR008063; Fas receptor.

InterPro; IPR01368; TNFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                        4040B7E0DB82454E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PKERC----
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:000165; P:immune response; IEA.
GO; GO:0007165; P:immune response; IEA.
InterPro; IPR001005; Myb_DNA_binding.
InterPro; IPR001005; Myb_DNA_binding.
InterPro; IPR001368; TNFR_c6.
PERM: PF00002; TNFR_c6, 2.
PRINTS; PR01680; PASRECEPTOR.
SWART; SM00208; TNFR; 3.
PROSITE; PS00037; MYB_I; UNKNOWN 1.
PROSITE; PS00062; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS050062; TNFR_NGFR_2; 3.
SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454
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PRINTS; PRO1680; FASRECEPTOR.
SMART; SMO0208; TNFR; 4.
PROSITE; PS00652; TNFR, NGFR 1; UNKNOWN 1.
PROSITE; PS50050; TNFR NGFR 2; 3.
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Query Match
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Q8VC17;
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                                                                                                                                                28VC17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 YHVKQVCSEHTG---TVCAP-CPPQTYTAHANGLSKCLPCGVCDPDMGLLTWQECSSWKD 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 YHVKQVCSEHTG---TVCAP-CPPQTYTAHANGLSKCLPCGVCDPDMGLLTWQECSSWKD 116
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                                                                                                                                                                                                                               60 --CICVTPEYHCGD---PQCKIC-KHYPCQPGQRVESQG----DIVFGFRCVACAMGTFS 109
                                                                                                                                                                                                                                                         110 -AGRDGHCRLWTNCSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTV----IFLVMAA 163
                                                                                                                                                                                                                                                                                                                                               172 LGGTQEECLPWTNCSARQ-QEVRRGTNSTDTTC-----SSQVVYYVVSILLPLVIVGAG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                              8 YGVSMLCVLDLGQPSVVEEPGCGPGKVQNGSGNNTRC--CSLYAPGK-----EDCPKER- 59
                                                                                                                                                                                                                                                                                                                                                                                                   164 CIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAEDACSFQFPEEERG-EQTEEK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                         225 IAGFLICTRRHLHTSSV-----AKELEPFQEQQEN-----TIRFPVTEVGFAETEEE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rickert S., Granger S.W., Ko M., Shukla D., Spear P.G., Kronenberg M.,
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                                                                                                      52; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                           Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 11.5%; Score 149.5; DB 2; Length 3 Best Local Similarity 26.9%; Pred. No. 4.7e-05; Matches 64; Conservative 34; Mismatches 89; Indels
                                                        11.8%; Score 154; DB 2; Length 27 27.7%; Pred. No. 1.9e-05; tive 28; Mismatches 92; Indels
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Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
38 Potential.
30171 MW; C4A7EADBEFC0521D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276 AA
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05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                    66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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275 AA;
                                                                                 Best Local Similarity
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SIGNAL
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                                                             Query Match
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                                                                                                  Matches
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ACALAR-WANN, 1128/BE-11787, WALAMER-WANN, 1128/BE-1247932, DOI=10.1073/pnas.242603899;
A Klausner R.D., Collins F.S., Wagner L.H., Derge J.G.,
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Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hasteh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Miching M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.A.,
Johes S.J., Marra M.J.,
Johes S.J., Marra M.J.,
Johes S.
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                                                             219 VIVGVGIAGFLICTRRHLHTSSVAKELEPFQQEQ----QENTIRFPVTEVGFAETEEE 272
169 TTVQLGLHIWQL-RRQHM----CPRETQPFABVQLSAEDACSFOFPEERRG-EQTEEK 220
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Straubberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022125; JAH-2125.1;
HSSP; Q92956; JUMA.
MGDJ; MGI:2675303; Thfrsf14;
GO; GO:0016020; Thermedrane; IEA.
GO; GO:001608915; P:ansmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
GO; GO:0006955; P:sigmal transduction; IEA.
FPERM; PFO0020; TNFR_CG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 196 AA; 21555 MW; 2AB3FF8905E260E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                 196 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last seq
01-WAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00208; TNFR; 3.
PROSITE; PS50050; TNFR_NGFR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00020; TNFR C6; 2.
PRINTS; PR01680; FASRECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Infrsf14 protein (Fragment)
Name=Infrsf14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
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Shimojima M., Miyazawa T., Ikeda Y., McMonagle E.L., Haining H.,
Akashi H., Takeuchi Y., Hosie M.J., Willett B.J.;
"Use of CD134 as a primary receptor by the feline immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                    virus.";
Science 0:0-0(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=CD40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q76LB4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   076LB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  076LB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SO DE REPERENTE DE LA PRIME DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 SGVVNQANPQNDTVCAPCQPGTYNSFNDAFTHCQSHTRCGDLGKEVKSAGTETTDAVCGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----IPEPLPTEQYGHLTVI-FLVMAACIFFLTTVQLGLHIWQLRRQHMCPRET----- 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CLPCRVCYSSSNQKVLREC-----EASSDRQCVCKT-GYXCTDDGCEHCLPVTLCPLG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |::|| ::||
-----WRAKRQSYMPANSSSPGIP 221
       ------- VVYYVV-SILLPLVI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 CGPGKVQNGSGNN--TRCCSLYAPGKEDCPKERCICVTPEYHCGDPQCKICKHYP-CQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 QRVESQGDIVFGFRCVACAMGTFSAGRDG--HCRLWTNCSQFGFLTMFPGNKTHNAVC--
                                                                          171 VOLGIHIWOL-RROHM----CPRETOPFAEVQLSAEDACSFOFPEEERG-EQTEEK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Felis silvestris catus (Cat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
NCBL_TaxID=9685,
                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Verrebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 10.7%; Score 139; DB 2; Length 318; Local Similarity 23.7%; Pred. No. 0.00045; nes 50; Conservative 28; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zou J., Secombes C.J.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ517804; CAD57165.1; -.
HSSP; Q92956; LJMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 AA; 35254 MW; 78F8135011283B43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 FISRCHWILPTSLWAGLVVTSLIIILICIY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----QPFAEVQLSAEDACSFQFPEEERGEQ 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEPAPSSFAPAELKFPTECNSHWSLDQKATE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 AA.
       94 GTQEECLPWTNCSAFQ-QEVRRGTNSTDTTCSSQ-
                                                                                                                                                                                                                                                                                                                  318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEAM; PF00020; TNFR c6; 2.
SMART; SM0208; TNFR; 4.
PROSITE; PS01186; BGF 2; 1.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 2.
PROSITE; PS50050; TNFR NGFR 2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO, GO:0004872; F:receptor activity; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour necrosis factor receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Head kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD134 homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=tnfr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q75SV8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q75SV8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
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                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275SVB
                                                                                                                                                                                                                                                                                  Q7T2H3
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                                                                                                                                                                                                                                                                                                                                                      ACCOCCOS ON THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 CVTPEYHCGDPOCKICKHYPCOPGORVESQGDIVFGFRCVACAMGTFSAGRDGHCRLWTN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 --TP-----TQDTVCR---CRPG--TEPQDGYDRGVDCAPCPPGHFSPGDDQACKPWTN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 CSQFGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLGLHIWQLR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TTP-----WETQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 EPGCGPGKVQNGSGNNTRCCSLYAPGKEDCPKERCICVTPEYHCGDPQCKIC-KHYPCQP 84
                                                                                                                                                                                                                                                                                                                                                                                                          29 CGPGKVQNGSGNNTRC-----CSLYAPG-----KEDC------PKERCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paralichthys olivaceus (Japanese flounder).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes;
Pleuronectoidei, Paralichthyidae, Paralichthys.
                                                                                                                                                                                                                                                                                                                                           75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 10.6%; Score 137.5; DB 2; Length 290; Similarity 22.9%; Pred. No. 0.00056; 46; Conservative 28; Mismatches 74; Indels 53
                                                                                                                                                                                                                                                                            10.6%; Score 138.5; DB 2; Length 270; 26.3%; Pred. No. 0.00042; ive 18; Mismatches 72; Indels 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 ROHMCPRETOPFAEVOLSAEDACSFOFP-EEERGEOTEEKCHLG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Park C., Hirono I., Aoki T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB081752; BAC87848.1; -.
GO; GO:0004872; Freceptor activity; IEA.
InterPro; IPR005209; EGF like.
InterPro; IPR001368; TNFR.c6.
SWART; SM00208; TNFR, 2.
PROSITE; PS01186; EGF 2; UNKNOWN_1.
PROSITE; PS01186; EGF 2; UNKNOWN_1.
SRQUENCE 290 AA; 32396 MW; B6FCF9E35305DFAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Park C., Hirono I., Aoki T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
EMBL, AB120892; BAJ1363.1; -.

GO, GO:0004872; F:receptor activity; IEA.

GO, GO:0004872; F:receptor activity; IEA.

InterPro; IPR01368; TMFR.c6.

SMART; SM00208; TNFR, 3.

PROSITE; PS00652; TNFR, MGFR.1; 2.

PROSITE; PS00509; TNFR, MGFR.2; 2.

SEQUENCE 270 AA, 28731 MW; 36A40BAD261140D1 CRC64;
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Last annotation update)
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SEQUENCE
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Strausberg R.;

Strausberg R.;

Submitted (WAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC049782; AAH49782.1; -.

GO: GO: 0005578; C:extracellular matrix (sensu Metazoa); IDA.

GO: GO: 0005615; C:extracellular space; TAS.

GO: GO: 0005615; C:extracellular space; TAS.

GO: GO: 0005615; C:extracellular space; TAS.

InterPro: IPR001488; Death.

InterPro: IPR001029; DEATH_like.

InterPro: IPR001368; TWRR_G6.

Rem; PF00020; TWRR_G6.

Rem; PF000208; TWRR; 4.

SMART; SM00005; DEATH; 1.

SMART; SM00005; DEATH, 1.

SMART; SM00005; TWRR; 4.

REMART; SM00005; TWRR; 4.

REMART; SM00005; TWRR, 4.

REMART; MOSITE; PS50017; DEATH_DMAIN; 1.

RESTRE: PS50050; TWRR_NGFR_1; 2.
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                                                                        126 GQWAKIKGNLTHDTVČESCPEGSFSTSHSWSSVČTKWTEC-ESGYHIQESGTNESDNICV 184
GQRVESQGDIVFGFRCVACAMGTFSAGR--DGHCRLWTNCSQFGFLTMFFGNKTHNAVCI 142
                                                                                                                     143 PEPLPTEQYGHLTVIFLVWAACIFFLTTVQ-LGLHIWQLRRQHMCPRETQPFAEVQLSAE 201
                                                                                                                                                     185 E---PPRHHGGL-----IACVVAVGSLAVVGLMVC-----LCKGET-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor necrosis factor receptor superfamily, member 11b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                            401 AA
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05-JUL_2004 (TrEMBLrel, 27, Last seq
05-JUL_2004 (TrEMBLrel, 27, Last ann
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                                                                                                                                                                                        202 DACSFQFPEEERGEQTEEKCH 222
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Name=Tnfrsf11b;
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TISSUE=Limb;
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                                                                                                                                                                                                                                                                                               76 ---IC------KHYPCQPGQRVESQGDIVFGFRCVACAMGTFS--AGRDGHC 116
                                                                                                                                                                                                                                                                                                                                                    101 HNRVCECEEGRYLEIEFCLKHRSCPPGSGVVQAGTPEQNTVCKKCPDGFFSGETSSKAPC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77
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GO; GO:004872; F:receptor activity; IEA.
GO; GO:0005031; F:tumor necrosis factor receptor activity; IEA.
GO; GO:0019221; F:tumor necrosis factor receptor activity; IEA.
GO; GO:0019221; P:tumor necrosis factor receptor activity; IEA.
InterPro; IPR011365; TNFR-cept_2.
InterPro; IPR011366; TNFR-cef.
PHRSF001928; TNFR-cf.
PHRSF001968; TNFR-2; 1.
PROSTITE; PS00652; TNFR NGFR.
PROSTITE; PS00652; TNFR NGFR.
PROSTITE; PS00652; TNFR NGFR.
FROSTITE; PS00652; TNFR NGFR.
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                                                                                                                                                                        45 CSLYAPG---KEDCP-KERCICV-----TPEYHCGD-----PQCK------
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.4%; Score 135.5; DB 2; Length 467; 21.1%; Pred. No. 0.0013; ative 33; Mismatches 95; Indels 137; Gaps
                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burgess S.C., Young J.R., Baaten B.J.G., Hunt L., Ross L.N.J., Parcells M.S., Kumar M.S., Tregaskes C.A., Lee L.F., Davison T.F.; "Marek's disease is a natural model for lymphomas overexpressing Hodgkin's disease antigen (CD30)."; Proc. Natl. Acad. Sci. U.S.A. 101:13879-13884 (2004).
                                                                                                                   48;
                                                  ch 10.5%; Score 136; DB 2; Length 401; 1 Similarity 28.2%; Pred. No. 0.001; 44; Conservative 10; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 467 CD30 protein.
467 AA; 51350 MW; F9AD4F77DEEC8588 CRC64;
401 AA; 45965 MW; 7C708E52EB46BA0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                      117 RLWINCSOFGFLIMFPGNKTHNAVCIPEPLPTEQYG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 RKHTNCSTFGLLLIQKGNATHDNVCSGNREATQKCG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potential
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Thesis (1998), Bristol University, UK.
EMBL, AJ276964; CAC79223.1;
HSSP; Q92956; LUMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2003 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD30 protein precursor.
                                                        Query Match
Best Local Similarity
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PubMed=15356338;
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Best Local Similarity
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SIGNAL
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63 PMDPDEDCMRCGPEQYLNQSPKPRCDACVLCTKEFDLVEKAPCSFNSSRVCECRPGMFCQ 122	KHYPCQPGQRVBSQGDIVFGFRCVACAMGTFSAGRDGHCRLWTNCSQ 124	STDVSCEECPPC	125 FGFLTMFPGNKTHNAVC141	183 LNKVAQGKGNATHDQVCTDQLPSYLTPDTSSIRITNETDDSDVLKRNANPVTLASILSSA 242	142IPEPLPTEQYGHLTVIFLVMAACIFFLTTVQLG-LHIWQLRRQHMCP 187	243 TTEIPGSTPEEEALAGTSPTLAKGETTTRGLVFWAVVLSVMVLPVGMLSFWQWKVCK 299	188 RETQPFAEVQLSAEDACSFQFPEEE 212	300 KRIFILKQKRSDLVDKYAKITLTT-DKCPEEE 330
63	78	123	125	183	142	243	188	300
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Search completed: October 26, 2005, 15:51:38 Job time : 118.299 secs

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October 26, 2005, 15:28:42 ; Search time 141.311 Seconds	(without alignments)	659.602 Million cell updates/sec
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Run on:		

Title:	US-09-545-998B-4
Perfect score:	1386
Sequence:	1 MAQHGAMGAFRALCGLALLCEEERGERSAEEKG

SRLGDLWV 241

2105692 segs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A Geneseq 16Dec04:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2000s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aaw37839 Amino aci	5 Human	Human	7 Human	_	Human	Human	Aab47054 Human PRO	Aab20115 Human imm		PR0364	2 Human	Aabs0910 Human PRO	Aae28161 Human TR1	Abu08442 Amino aci	Aao16574 Human tum	Aao23091 Human ene	Adn39966 Cancer/an	Adh43131 Human TNF	Adl91869 Human PRO	Human	Adp55559 Human PRO	Adt94287 Human PRO	Adr46662 Cancer-as	Aay44825 Human mol
	ΩI	AAW37839	AAY06605	AAB33431	AAY71467	AAB27651	AAY95895	AAB24409	AAB47054	AAB20115	AAB53090	AAB47289	AAB50982	AAB50910	AAE28161	ABU08442	AA016574	AA023091	ADN39966	ADH43131	ADL91869	AD020289	ADP55559	ADT94287	ADR46662	AAY44825
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æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.7	97.2
	Score	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1386	1382	1347
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This is the amino acid sequence encoding the human 112C2 T cell protein. The 112C2 proteins are expressed in thymus cells and are induced on T cells and spleen cells following activation. Engagement of 112C2 atimulates proliferation of T cell clones, antigen-specific proliferation and cytokine production by T-cells, and potentiates T cell expansion or apoptosis. The products can be used in the treatment of conditions associated with abnormal physiology or development, including abnormal proliferation, e.g. cancerous conditions or degenerative conditions. They can be used in the regulation or development of haematopoietic cells,

. 9.9

Isolated 312C2 T cell gene - used to develop products for treating, cancers, auto-immune disorders, transplantation rejection and other cell disorders.

Claim 2; Page 59-60; 71pp; English

Aao16576 Human tum		Aay95879 Human tum	Aay52158 Tumour ne	Human	Abu08439 Amino aci	Human	Human	Human	Human	Ado20305 Human PRO	Human	Aao23094 Human ene	Aaw37840 Truncated	Aao16577 Human tum	Aao23099 Human ene	_	Aay52160 TR11SV2 a	Aae28160 Human TR1	Abu08441 Amino aci
AA016576	AA023093	AAY95879	AAY52158	AAE28158	ABU08439	AA016575	ADA09435	AA023092	ADH43105	AD020305	ABB89386	AA023094	AAW37840	AA016577	AA023099	AAY95881	AAY52160	AAE28160	ABU08441
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235	235	234	234	234	234	234	234	234	234	234	246	228	228	228	228	240	240	240	240
97.2	97.2	95.4	95.4	95.4	95.4	95.4	95.4	95.4	95.4	95.4	94.3	93.3	93.1	93.1	93.1	92.0	92.0	92.0	92.0
1347	1347	1322.5	1322.5	1322.5	1322.5	1322.5	1322.5	1322.5	1322.5	1322.5	1306.5	1293.5	1290.5	1290.5	1290.5	1274.5	1274.5	1274.5	1274.5
26	27	28	29	30	31	35	33	34	35	36	37	38	68	40	41	42	43	44	4.5

ALIGNMENTS

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Human 312C2 T cell protein; thymus cell; spleen cell; T cell; antigen-specific T cell proliferation; cytokine production by T-cell; apoptosis; cancer; haematopoietic cells; lymphoid cell; autoimmune disorders.
                                                            Amino acid sequence of the human 312C2 T cell protein.
                                                                                                                                                                                                                      Zlotnik A;
              Ä
              AAW37839 standard; protein; 241
                                                                                                                                                                               96US-00689943
96US-0027901P
                                                                                                                                                                 97WO-US013931
                                            (first entry)
                                                                                                                                                                                                                     Gorman DM, Randall TD,
                                                                                                                                                                                                       (SCHE ) SCHERING CORP.
                                                                                                                                                                                                                                     WPI; 1998-159534/14.
N-PSDB; AAV19153.
                                                                                                                                 WO9806842-A1.
                                                                                                                    Homo sapiens.
                                                                                                                                                                14-AUG-1997;
                                           28-JUL-1998
                                                                                                                                                                                16-AUG-1996;
07-OCT-1996;
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                              AAW37839;
RESULT 1
       AAW37839
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responses
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e.g. lymphoid cells which affect immunological responses, e.g. autoimmune disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor necrosis factor receptor homologue - useful for, e.g. modulating apoptosis and NF-KB activation and proinflammatory or autoimmune
                                                                                                                                                                                                                                                                                                                                                   121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPFAEPLGWLTVVLLAVAACVLLL
                                                                                                                                                                                                                                                                                                                                                                                                             TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW
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                                                                                                   Length 241;
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                                                                                               Score 1386; DB 2;
Pred. No. 2.2e-101;
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/note= "transmembrane domain"
                                                                                 100.0%; Scc. 100.0%; Pred. No. ... 0; Mismatches
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note= "signal peptide"
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/note= "mature protein"
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                                                                                                                                     Matches 241; Conservative
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                                                                                                                   Local Similarity
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                                                               Sequence 241 AA;
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Best Local S
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Peptide
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                                                                                                tumour necrosis factor receptor family. The sequence was deduced from a bone marrow cDNA clone (see AAX87670). Methods for the recombinant production of PRO364 polypeptides, e.g. in CHO, Escherichia coli or yeast host cells, are provided. Claimed polypeptides comprise amino acids 1-241, 1-X, 26-241 (i.e. the mature protein) and 26-X of the present PRO364 polypeptides are useful for modulating apoptosis, NF-KB activation and proinflammatory or autoimmune responses in mammalian cells (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                          chimeric molecules comprising a PRO364 polypeptide fused to a heterologous sequence such as epitope tag or immunoglobulin Fc region are also claimed. PRO364 can be used in assays to identify other proteins or molecules involved in binding interactions. This is useful for identifying inhibitors or agonists of receptor/ligand binding. The PRO364 polypeptides may also be combined with an agent that is cytotoxic, chemotherapeutic or a growth inhibitor. PRO364 antibodies are useful in diagnostic methods, purification methods and also in therapy, e.g. as inhibitors
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                                                                    The present sequence represents human PRO364, a novel member of the
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Claim 17; Fig 2A; 104pp; English.
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Matches 241; Conservative
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Lu Y, Pe
Tumas D,
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            WO200053758-A2
                                                20-APR-1999;
28-APR-1999;
04-MAY-1999;
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       Homo sapiens
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                         02-MAR-2000;
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                   14-SEP-2000
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05-OCT-1
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29-NOV-1
30-NOV-1
                                                                 23-JUN-5
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                                                                                   08-SEP-
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graft rejection; graft-versus-host-disease. 99US-0132371P. 99US-0134287P. 99WO-US012252. 99US-0141037P. 99US-0144758P. 99US-0145698P. 99US-0146222P. 99WO-US023089. 99US-0162506P. 99WO-US028214. 99WO-US028313. 99WO-US028409. 99WO-US020111. 99WO-US020594. 99WO-US028634. 99WO-US020944. 2000WO-US000277. 2000WO-US000376. 99US-0128849P. 99WO-US021090 99WO-US031274 2000WO-US004341 2000WO-US004414 99US-0131445P 99WO-US021547 99WO-US028301 99WO-US028551 99WO-US028564 99WO-US028565 99WO-US030095 99WO-US030999 2000WO-US003565 2000WO-US005841

KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Pan J, Pennica D, Shelton DL, Smith V;
, Watanabe CK, Wood WI, Yan M; Ashkenazi AJ, Baker KP,

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.

Claim 33; Fig 36; 309pp; English

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoathritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic

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                       immune—mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, utcimmune or immune-mediated skin diseases, allergic diseases, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease. AACS8397 to AACS8578 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACS879 to AACS8642 and AAB3414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
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autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus,
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100.0%; Pred. No. 2.2e-101;
tive 0; Mismatches 0;

    .11
    'note= "N-myristoylation site"

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/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY71467 standard; protein; 241 AA.
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/note= "N-
118. .124
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/note= "N
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Matches 241, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence 241 AA;
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The present invention relates to methods for stimulating or inhibiting angiogenesis and cardiovascularization. The methods involve the use of pharmaceutical compositions based on the following proteins, PRO179, PRO218, PRO344, PRO846, PRO1760, PRO205, PRO321, PRO341, PRO849, PRO847, PRO846, PR
181 TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
                                                                                                                                                                                                                                                                                                                             Cardiovascular; endothelial; angiogenic disorder; PRO179; PRO238; PRO364; PRO844; PRO846; PRO1760; PRO205; PRO3121; PRO8333; PRO840; PRO877; PRO878; PRO879; PRO882; PRO885; Gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel PRO polypeptides and agonists and antagonists of them, used to diagnose and treat cardiovascular, endothelial and angiogenic disorders.
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Paoni NF, Pitti RM;
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    .25
    /label= Signal peptide

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                                                                                                                                                                          AAB27651 standard; protein; 241 AA.
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05-JAN-2000; 2000WO-US000219.
18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004341.
22-FEB-2000; 2000WO-TS004342.
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Williams PM,
                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                           Human protein PRO364.
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Watanabe CK,
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01-SEP-1999;
15-SEP-1999;
30-NOV-1999;
30-NOV-1999;
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                                                                                                                                                                                                                  AAB27651;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New composition useful for inhibiting neoplastic cell growth and for treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or their
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                                                                                                                                                                          166. .177
/note= "Prokaryotic membrane lipoprotein lipid attachment
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100.0%; Pred. No. 2.2e-101;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                         'note= "Leucine zipper pattern"
                                                            46. .150
note= "Asn is N-glycosylated"
56. .162
                                        note= "N-myristoylation site"
    "N-myristoylation site"
                                                                                                                       note= "N-myristoylation site"
                                                                                                                                                           Transmembrane domain
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98US-0113296P.
99US-0144758P.
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/label= Tr
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        'note=
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N-PSDB; AAD01240.
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Best Local Similarity
Matches 241; Conserv
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22-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tumor necrosis factor receptor-like proteins useful for diagnosis, prevention and treatment of disease states associated with aberrant cell survival such as autoimmune disease and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of human tumour necrosis factor receptor-
like protein TR11 (see also AAY95879), a novel protein showing identity
to murine glucocorticoid induced tumour necrosis factor receptor family-
related gene. The invention provides highly conserved TR11, TR115V1 and
TR115V2 proteins (see AAY95879-81), as well as vectors, host cells and
recombinant methods for their production. TR11, TR115V1 and/or TR115V2
polypeptides are useful for treating, preventing, prognosis and/or
diagnosis of an immunodeficiency, especially common variable
                                                            61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
                                                                                                                                             MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                                                                                                                                         TR11; human; tumour necrosis factor receptor-like protein;
immunodeficiency; autofmmune disease; rheumatoid arthritis;
immunosuppressive; antirheumatic; antiarthritic; haemostatic;
dermatological; antiinflammatory; therapy; diagnosis; mutein; mutant.
                              Gaps
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                                                                                                                                                                                                                                                                                                                                                    necrosis factor receptor-like protein TR11 mutein.
          Length 241;
                             Indels
        ; Score 1386; DB 3;
; Pred. No. 2.2e-101;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, 294-295; 278pp; English
                                                                                                                                                                                                                                                                                           AAY95895 standard; protein; 241 AA.
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99US-0134172P.
99US-0144076P.
          100.0%;
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                                                                                                                                                                                                                                                                                                                                  (first entry)
    Query Match
Best Local Similarity 100."
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                                                                                                                                                                                                                                                                                                                                                       Human tumour
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                                                                                                                                                                                                                                                                                                                                  20-NOV-2000
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AAY95895
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immunodeficiency, X-linked agammaglobulinemia, severe combined immunodeficiency (SCID), Wiskott-Aldrich syndrome or X-linked immunoglobulin deficiency with hyper IgM. TR11, TR11SV1 and/or TR11SV2 antagonists (e.g. antibodies) are used to treat, prevent, prognose and/or diagnose an autoimmune disease, especially rheumatoid arthritis, systemic lupus erythematosus, thrombocytopenia purpura or IgA nephropathy. The polypeptides, polynucleotides and/or antibodies can be administered to cells in vitro, ex vivo or in vivo or to a multicellular organism. Soluble forms of the polypeptides may also be used. Methods for screening for agonist/antagonist compounds are also provided
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
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                                                                                                                                                                                                                                                                                                                                                                                                              61 YPGEECCSEWDCMCVQPBFHCGDPCCTTCRHPPCPPGQVQSQGKKSFGFQCIDCASGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL
                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                         100.0%; Score 1386; DB 3; Length 241; 100.0%; Pred. No. 2.2e-101; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human PRO364 protein sequence SEQ ID NO:117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB24409 standard; protein; 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0123957P.
99US-0131445P.
99UG-0134287P.
99US-0141037P.
99US-0144758P.
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99US-0115554P.
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                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 241; Conservative
                                                                                                                                                                                                                                                          Sequence 241 AA;
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16-DEC-1998;
12-JAN-1999;
08-MAR-1999;
12-MAR-1999;
28-APR-1999;
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20-JUL-1999;
26-JUL-1999;
01-SEP-1999;
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02-JUN-1999
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                                                                                                                                                                                                                                                                                                    Query Match
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99WO-US020111

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This sequence represents PRO364 polypeptide, which is a human glucocorresponding ligand (horTRL), PRO475, is given in ABA47056. PRO364 and PRO175 may be used in a mixture with a cardiovascular, endothelial, angiogenic or angiostatic disorder. The PRO364 cDNA sequence was isolated from an expressed sequence tag (EST) database as having the phomology to members of the tumour necrosis factor receptor (TNPR) family of polypeptides. The PRO175 cDNA sequence was isolated from a library of comparting an effective amount of PRO364 or PRO175 cr their antagonists is useful for treating cardiac hypertrophy (which is antagonists is useful for treating cardiac hypertrophy (which is an elevated level of PGF 2alpha), trauma, a cancer, or age-related macular degeneration in a human. Administering a therapeutically effective amount of an antibody that binds PRO364 or PRO175 is useful for inhibiting angiogenesis induced by PRO364 or PRO175 in a human suffering from a tumor or a retinal disorder. PRO364 or PRO175, or their antagonists, are useful for vascular-related drug targeting or as therapeutic cancer, or age antagonists, are useful for recatment or prevention of atheroscales. PRO364 or PRO175, or their antagonists, are useful for recatment or prevention of atheroscales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypertension, inflammatory vasculitides, Reynaud's disease, aneurysms, arterial restenosis, thrombophlebitis, tumor angiogenesis, gut protection or regeneration and treatment of lung or liver fibrosis, periodontal
              PROJ64; human; glucocorticoid-induced tumor necrosis factor; receptor; human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy; human umbilical vein endothelial cell; HUVEC; cardiac hypertrophy; myocardial infarction; PGF 2alpha; trauma; cancer; angiogenesis; age-related macular degeneration; antibody; periodontal disease; vascular-related drug targeting; atherosclerosis; hypertension; inflammatory vasculitides; Reynaud's disease; aneurysm; arterial restenosis; thrombophlebitis; tumor angiogenesis; lung; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Composition for diagnosing and treating cardiovascular, endothelial and angiogenic disorders, comprises a PRO364 or PRO175 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases, attraction of bone-forming cells, central and peripheral nervous system disease and neuropathies and rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                      162. .180
/note= "Potential transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 1386; DB 4; Best Local Similarity 100.0%; Pred. No. 2.2e-101; Matches 241; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                            l. .26
/note= "Potential signal peptide"
                                                                                                                                                                          fibrosis; neuropathy; rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                   /note= "N-glycosylated"
                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUL-2000; 2000WO-US018867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams PM, Gerritsen ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-138257/14.
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                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUL-1999;
                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenesis and cardiovascular, endothelial or angiogenesis and cardiovascular by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and dispnosis of diseases associated with inappropriate PRO expression such as cardiovascular, andothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCs) and vectors containing them and the PRO polypeptide may be used to treat disorders associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24188 to AAB24415 represent
                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes nucleic acids encoding PRO polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTGTDARCCRVHTTRCCRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotide and protein sequences used in the exemplification of the
                                                                                                                                                                            Hillan KJ;
Kuo SS, Paoni NF;
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                                                                                                                                                                          Gerber H,
Klein RD,
Wood WI;
                                                                                                                                                                          , Ferrara N,
T, Gurney AL,
Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB47054 standard; protein; 241 AA.
                                                                                                                                                                                                                                                                                                                                                                                               Claim 72; Fig 44; 315pp; English.
                99WO-US020944.
99WO-US021090.
99WO-US021547.
99WO-US023089.
  99WO-US020594
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                                                                                                                                                                            Baker KP,
lowski PJ,
                                                                                                                                                                                                Goddard A, Godowski PJ
Smith V, Watanabe CK,
                                                                                                                                       (GETH ) GENENTECH INC.
                                                                                                                                                                                              Godowski
                                                                                                                                                                                                                                                       WPI; 2000-412154/35.
N-PSDB; AAA77604.
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                                                                                              29-OCT-1999;
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  08-SEP-1999
                                                       15-SEP-1999
                                      15-SEP-1999
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                                         120
                                                       180
                                                                                                                                                                                                                      PRO364; UNQ319; human; immune disease; autoimmune disease; antirheumatic;
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                                                               YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
                                  61 YPGEECCSEMDCMCVQPBFHCGDPCCTTCRHHPCPPGQVQSQGKFSFGFQCIDCASGTF
                                                       SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL
                                                                                  TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW
                                                                                                                                                                                                                            antiarthritic; antiinflammatory; antiansemic; immunosuppressive; antithyroid; antidiabetic; neuroprotective; hepatotropic; virucide; dermatological; antipsoriatic; antiasthmatic; antiallergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "leucine zipper pattern'
                                                                                                                                                                                                                                                                                                                 8. .14
/note= "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                                              /note= "N-myristoylation site"
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                                                                                                                                                                                                                                                                                                          "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                             "N-myristoylation
                                                                                                                                                                                                                                                                                                                                      "N-myristoylation
                                                                                                                                                                                                                                                                                     1. .25
/label= Signal peptide
                                                                                                                                                                                                                                                                                                                                                    /label= Mature_protein
                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                               AAB20115 standard; protein; 241 AA
                                                                                                                                                                                                         Human immunostimulant PRO364,
                                                                                                                                                                                                                                                                                                                                                                                                  .128
                                                                                                                                                                                                                                                                                                                                                                                                                  .150
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The present sequence is that of novel human immunomodulator PR0364 (100019), as deduced from CDNA (see AAR3007) isolated from a small intestinal library. PR0364 (26 kDa, pI 6.34) shows sequence homology to mouse GITR protein and may be lite human counterpart. The invention counterpart proteins of see AAR30056-62) encoding in ovel human PR0 proteins (see AAB20108-20) including PR0364. Claimed compositions comprising these proteins or their agonists are useful for increasing infiltration of inflammatory cells into a tissue of a mammal, stimulating comprising a nammal in response to an antigen. Claimed compositions or enhancing an immune response, or increasing the proliferation of I.

Or captusing a PR0 polypeptide or its antigen. Claimed compositions comprising a PR0 polypeptide or its antigen. Claimed compositions or enhancing an immune response to an antigen. Claimed compositions comprising a PR0 polypeptide or its antigen. Claimed compositions or call disorder, involves administering a PR0 polypeptide, an agonist call processor antibody or an antagonist antibody. The disorder is selected from antibody or an antagonist antibody. The disorder is selected from systemic lupus erythemacosus, rheumatory polypethide, an agonist call proposition and processor of systemic athritis, spondyloarthropathy, systemic selected from systemic athritis, succionarie, autoimmune heamlylic antibody and the systemic composition and processor (such as multiple sclerosis), immunelylatis, inflammatory bowel disease (such as multiple sclerosis), antendent control of seases, gluth and psoriasis), allergic diseases (such as multiple sclerosis), immunelylated skin diseases of the lung and transplantation associated diseases (such as graft rejection and graft-versus-host comprise detecting the level of separession of the PRO polypeptide, vectors, host cells arising proder such as graft rejection and graft-versus-host cells in amethod of stimulating the proliferation of T lymphocytes using PR0364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGHEGHCKPWIDCIQFGFLIVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 New PRO polypeptides, nucleic acids and (ant)agonists, useful for diagnosing and treating immune-related disorders, such as multiple sclerosis, rheumatoid arthritis and diabetes.
                                                                                                                                                                                              PJ;
Tumas I
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                                                                                                                                                                                                      Godowski PJ
Pitti RM,
                                                                                                                                                                               Hillan KJ, Mark MR, Marsters SA, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Fig 16; 127pp; English.
15-MAR-2000; 2000WO-US006884.
                                                                   99US-0144758P
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Best Local Similarity 100.
Matches 241; Conservative
                                                                                                                                      (GETH ) GENENTECH INC
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Watanabe CK,
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25-JAN-2001

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Homo sapiens
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TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid for producing a PRO polypeptide, analyzing genetic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO protein, agonists or antagonists of a PRO protein, and
                                                                                                                                                                                                             Human; angiogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; angiogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;
Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                        Human angiogenesis-associated protein PRO364, SEQ ID NO:142
                                                                                                                       AAB53090 standard; protein; 241 AA.
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                                                                                                                                                                                                                                                                                 gene therapy; transgenic animal
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99US-0145698P.
99WO-US020111.
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compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying medulators of PRO corpsision or activity, diagnosing a cardiovacular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a comparison or a trace of the administration of a PRO protein, PRO nucleic acid, or PRO agonist or antagonist; a retroviral gene therapy vector comprising a promise acid, and methods of inhibiting or stimulating endothelial call growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO administration of a PRO protein, or an agonist or antagonist, proceeding, and the administration of a PRO protein, or an agonist or antagonist, thereof. Or agonists and PRO antagonists may be used as therapeutic agents to treat cardiovascular, endothelial or angiogenic disorders, such as approached and proteins, who agonists and proteins, wounds, cancer, Alzheimer's disease, Huntington's disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to analyse genetic disorders, and in genee therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated PRO polypeptide useful in treating and diagnosing a cardiovascular, endothelial or angiogenic disorder e.g. cancer, diabetes mellitus, myocardial infarction, arthritis.
                                                                                                                                                                                                                                                                                                        166. .177
/label= Prokaryotic membrane lipoprotein attachment site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gurney AL;
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Paoni NF, Pitti RM,
                                                                                                                                                                                                                                                                                 162. .180
/label= Potential transmembrane domain
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label= N-linked glycosylation site
                                               Bite
                                                                                                                                                                                 118. .124
/label= N-myristoylation site
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/label= N-myristoylation site
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label= N-myristoylation site
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label= N-myristoylation
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|label= N-myristoylation
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/label= N-myristoylation
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/label= Signal peptide
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Location/Qualifiers
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2000WO-US008439.
2000WO-US013705.
2000WO-US014941.
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2000WO-US005004
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/label= N-
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N-PSDB; AAC85947.
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                                                                                                                                                                                                                                                                                                          Binding-site
                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-2001
                                                                                                           Protein
            Peptide
                                                                                                                                                                                                                                                                                    Domain
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include diabetes mellitus, osteoporosis, ischaemia, hypertension, rheumatoid arthritis, Crohn's disease, atherosclerosis, psoriasis, acidometriosis, anglina, neoplasms, periodontal disease, bone and cartilage repair, Alzheimer's disease, Parkinson's disease, Huntington's disease, amylotrophic lateral sclerosis, and stroke
                                                                                                                                                                                                                                                                             180
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                                                                                                                                                                                                                                                                                                                                                  121 SGGHEGHCKFWIDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL
                                                                                                                                                                                                                                                                                                                                   TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW
                                                                                                                                                                1 MAQHGAMGAFRALCGIAILCALSIGQRPTGGPGCGPGRILLGTGTDARCCRVHTTRCCRD
                                                                                                                                                                                 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
                                                                                                                                                                                                                                                61 YPGEBCCSEWDCMCVQPBFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
                                                                                                                                                                                                                                                                             SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL
                                                                                                                                        Gaps
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                                                                                                            Length 241;
                                                                                                                                        Indels
                                                                                                            100.0%; Score 1386; DB 4;
100.0%; Pred. No. 2.2e-101;
tive 0; Mismatches 0;
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99US-0141037P.
99US-0144758P.
99US-0145698P.
99US-0146222P.
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99WO-US030095.
2000WO-US000219.
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18-FEB-2000; 2000WO-US004341.
18-FEB-2000; 2000WO-US004342.
24-FEB-2000; 2000WO-US005004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001 (first entry)
                                                                                                                              Best Local Similarity 100.
Matches 241; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO364 protein.
                                                                                                                            Similarity
                                                                                    Sequence 241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           241 V 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JAN-2000;
06-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-SEP-1999;
30-NOV-1999;
30-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-DEC-1999;
16-DEC-1999;
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                                                                                                                 Query Match
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antidiabetic; nootropic; neuroprotective; hepatotropic; virucide;
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                                                                                        WO200073452-A2.
                antiallergic;
hepatobiliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ashkenazi AJ,
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Watanabe CK,
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06-JAN-2000)
11-FEB-2000)
11-FEB-2000)
11-FEB-2000)
22-FEB-2000)
24-FEB-2000)
24-FEB-2000)
01-MAR-2000)
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02-DEC-1999;
02-DEC-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-MAR-2000;
15-MAR-2000;
                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-2000;
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                                                                                                                                                                                                                                                                                          29-OCT-1999;
                                                                                                                                                                                                                                                               .5-SEP-1999;
                                                                                                                      07-DEC-2000
The present sequence is one of seventeen novel PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to etimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 YPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVFGSPPAEPLGWLTVVLLAVAACVLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL
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                                                                                                                      ', Gerber H, Gerritsen ME;
', Kuo SS, Mark MR, Marsters SA;
Williams PM, Wood WI;
                                                                                                                                                                                                                                Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, PRO; antinflammatory, dermatological, antiarthritic,
antirheumatic, cardiant, antianaemic, immunosuppressive, antithyroid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1386; DB 4; Length 241; 100.0%; Pred. No. 2.2e-101; ive 0; Mismatches 0; Indels 0
                                                                                                                          Ferrara N,
                                                                                                                                      PJ, Gurney AL,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AABS0910 standard; protein; 241 AA.
                                                                                                                                                                                                                                                                                              Claim 71; Fig 8; 182pp; English.
            10-WAR-2000; 2000WO-US006319.
15-WAR-2000; 2000WO-US006884.
21-WAR-2000; 2000WO-US007532.
30-WAR-2000; 2000WO-US008439.
2000WO-US005841
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                                                                                                                      Baker KP,
dowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 241; Conservative
                                                                                                                                                                                                                                                               disorders in a mammal.
                                                                                        (GETH ) GENENTECH INC.
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                                                                                                                                     Goddard A, Godowski
Paoni NF, Pitti RM,
                                                                                                                                                                                     2001-025251/03
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                                                                                                                                                                                                    N-PSDB; AAC90566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 241 AA;
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                                                                                                                      Ashkenazi AJ,
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PRO polypeptides, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic ansemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems (such as multiple sclerosis, idiopathic demyelinating polyneuropathy or Guillain-Barre syndrome, and chronic inflammatory demyelinating polyneuropathy), hepatobiliary diseases (such as infectious, autoimmune chronic active hepatitis, primary biliary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thirty three nucleic acids encoding PRO polypeptides which are useful ithe diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis
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Shelton DL,
antiasthmatic; immune related disorde disease; allergy.
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Kabakoff RC,
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--- C, Henzel W, F
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99US-0144732P.
99US-0144758P.
99US-0146222P.
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99WO-US028313.
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2000WO-US005004
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Wood WI;
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and diabetes mellitus.
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                                                                                                                                                                                                                                                                                                                                                                                                    120
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             inflammatory bowel disease, gluten-sensitive enteropathy and Whipple's disease, autoimmune or immune-mediated skin diseases (such as bullous skin diseases, autoimmune or immune-mediated skin diseases (such as bullous allergic diseases erch as acthma, allergic rhinitis, atopic dermatitis, food hypersensitivity and urticaria), immunological diseases of the lung then as eosinophilic pneumonias, idiopathic pulmonary fibrosis and hypersensitivity pneumonitis), transplantation associated diseases including graft rejection and graft-versus-host diseases
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                                                                                                                                                                                                                                                                                                                                                                                    61 YPGEECCSEWDCMCVQDEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTF
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                                                                                                                                                                                                                                                     Gaps
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cirrhosis, granulomatous hepatitis and sclerosing cholangitis)
                                                                                                                                                                                                                 4; Length 241;
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                 100.0%; Score 1386; DB 4;
100.0%; Pred. No. 2.2e-101
Live 0; Mismatches 0;
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98US-00176200.
99US-0121648P.
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                                                                                                                                                                                                                                                         Matches 241; Conservative
                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                  Sequence 241 AA;
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24-FEB-1999;
13-MAY-1999;
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The present invention relates to novel antibodies or their portion which specifically bind tumour necrosis factor (TNF) receptor-related protein specifically bind tumour necrosis factor (TNF) receptor-related protein splice variants, TR11SV1 or TR11SV2. Sequences of the invention are conditions associated with aberrant expression and/or activity of TR11, TR11SV1 and TR11SV2 polypeptides, e.g., autoimmune diseases such as autoimmune haemolytic anaemia, allergic encephalomyelitis, multiple colleges, systemic lupus erythematosus, Goodpasture's syndrome, diabetes mellitus, rheumatoid arthritis, Sjogren's syndrome, scleroderma with anti-collagen antibodies, urticaria, conditions such as respiratory disorders (e.g. asthma, allergy), allergic reactions such as respiratory calisorders (e.g. asthma, allergy), allergic reactions such as asthma, graft-versus-host-disease, transplantation rejections, type II collagen-conditions active cancer), cardiovascular disorders (atherosclerosis, myocarditis), gastrointestinal disorders (atherosclerosis, myocarditis), gastrointestinal conditions and disorders (e.g. traumatic brain nigury, Alzheimer's disease, stroke) and disorders characterised by inflammation (e.g. gout, trauma, septic shock). They are used for modulating haemostatic or thrombolytic activity and thus is used for treating blood coagulation disorders, the blood platelet disorders (e.g. thrombocytopaenia) or wounds resulting from trauma, surgery or other causes. Polymucleotides of the invention are useful in gene therapy and immuno therapy. The present sequence is human TR11 receptor protein
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                                                                                                                                                                                                         Novel antibody or its portion which specifically binds to two tumor necrosis factor receptor-related protein splice variants, TR11SV1 and TR11SV2, useful for treating autoimmune hemolytic anemia, and Goodpasture's syndrome.
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16-JUL-1999; 99US-0144076P.
23-FEB-2000; 2000US-00512363.
28-JUL-2000; 2000US-0221577P.
                                                                                      (HUMA-) HUMAN GENOME SCI INC
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Homo sapiens.
                            antiallergic
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    13-JUN-2003
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21-0CT-1998;
                                                          16-JUL-1999;
                                         07-JAN-2003
                                                      24-FEB-1999
                                                        13-MAY-1999
                                                                                                                       polypeptide
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The present invention relates to the isolation of novel members of the tumour necrosis factor (TNP) family of receptors, referred to as TNF creeptor-related proteins and designated TR11, TR11SV1 and TR11SV2 represent splice variants of TR11. The invention also discloses the polymucleotide sequences encoding the TR11 receptors, and a creeptors in mammals. The method of the invention is useful for inhibiting the binding of endokine-alpha binding to endogenous endokine-alpha creeptors in amammal, preferably humans. The method is useful for inhibiting or preventing immunodeficiency (SCID) x linked, Bruton's disease (e.g. severe combined immunodeficiency (SCID) x linked, Bruton's disease.

O'sgammaglobulinaemia), and autoimmune diseases (e.g. systemic lupus erythematosus (SLB), rheumatoid arthritis, dermatitis, allergic conversed to the present sequence represents human TR11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting binding of endokine-alpha to endogenous endokine-alpha receptors in a mammal, by administering to a mammal a fragment of human tumor necrosis factor receptor-related protein.
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                                                                                                                                                                               endokine-alpha; endokine-alpha receptor; immunodeficiency disease; severe combined immunodeficiency-X linked; SCID-X linked; SLE; Bruton's disease; dysgammaglobulinaemia; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; dermatitis; allergic encephalomyelitis; immunostimulant; dermatological; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;
                                                                                                                                               necrosis factor receptor family; TNF receptor; TR11
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                                                                           Amino acid sequence for human TR11 polypeptide.
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98US-00176200.
99US-0121648P.
99US-0134172P.
99US-0144076P.
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(first entry)
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Matches 241; Conservative
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121 SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLL 180
                                                                                                                                 Search completed: October 26, 2005, 15:47:40
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein October 26, 2005, 15:51:55; Search time 115.618 Seconds (without alignments) 870.278 Million cell updates/sec Run on:

US-09-545-998B-4

1386 1 MAQHGAMGAFRALCGLALLC......EEERGERSAEEKGRLGDLWV 241 Title: Perfect score:

Sequence:

1862994 seqs, 417510619 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 28, Appl									Sequence 2, Appli	Sequence 2, Appli
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DB	6	13	14	14	15	17	20	16	σ	14	14
% Query Match Length DB ID	241	241	241	241	241	241	241	240	234	234	234
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.7	95.4	95.4	95.4
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Sequence 1762, Ap	ģ	9	9 9	4	9	4	0	6	,	N	_	_	N	-	4,	-	~	۵, 4	o i	=	quence 13	N	equence 2	equence 9	equence 2	eguence 2	equence 1	Sequence 160, App	equence 1	_	_	_	Sequence 588, App
S US-10-264-237-1762	US-09-915-593-6	-10-283	4 US-10-277-966-6	593-	5-10-283	US-10-277	3 US-10-116-378-26		US-09-915-593-7	0-116	-10-283-105	4 US-10-277-966-7	US-10-959-537-2	0-998-60-SD	US-10-369-300-	0-027-199-	4 US-10-067-122-2	0-981-352	US-09-739-394-9	US-09-826-212-11	-932-	0 US-09-877-336-2	09-877-338	3 US-10-097-330-9	-10-027-	4 US-10-170-997-2	US-10-186-	US-10-207-655-1	US-10-418-242-1	US-10-646-308-1	US-10-755-88	US-10-748-112-1	6 US-10-723-860-588
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ALIGNMENTS

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US-05-915-593-28
Sequence 28, Application US/09915593
Fatent No. US20020098525A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
FILE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
FILE REPRENCE: PF936F2
CURRENT APPLICATION NUMBER: 60/09/21, 577
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 2000-02-23
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR PILING DATE: 1999-02-24
PRIOR PILING DATE: 1999-02-24
PRIOR PILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-10-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LEASTH: 241
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CRGANISM: Homo sapiens
US-09-915-593-28
RESULT 1
US-09-915-593-28
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RESULT 4
US-10-277-966-28
Sequence 28, Application US/10277966
Publication No. US20030153499Al
GENERAL INFORMATION:
                                                                                                                              Sequence 28, Application US/10283105
Publication No. US20030138426A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 241; Conservative
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SOFTWARE: Patentin version
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US-10-283-105-28
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US-10-283-105-28
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LENGTH: 241
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                                                                          1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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Publication No. US20020150993A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin
APPLICANT: Biti, Robert M.
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Nood, William
APPLICANT: Nood, William
APPLICANT: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: P1206R1
CURRENT PAPPLICATION NUMBER: US/10/116,378
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/247,225
PRIOR PILING DATE: EARLIER FILING DATE: 1999-02-09
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 3
LENGTH: 241
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100.0%; Score 1386; DB 9; Length 241; 100.0%; Pred. No. 1.1e-106; ive 0; Mismatches 0; Indels 0
Query Match
Best Local Similarity 100.0
Matches 241; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
TITLE OF INVENTION: Humber: US/10/283,105
CURRENT FILING DATE: 2002-10-30
PRIOR PELICATION NUMBER: 09/915,593
PRIOR FILING DATE: 2001-07-27
PRIOR PILING DATE: 2000-07-28
PRIOR PLICATION NUMBER: 09/512,363
PRIOR FILING DATE: 2000-02-23
PRIOR PLICATION NUMBER: 60/134,172
PRIOR PLICATION NUMBER: 60/134,172
PRIOR PLICATION NUMBER: 09/116,200
PRIOR PLICATION NUMBER: 09/116,200
PRIOR PLING DATE: 1999-02-44
PRIOR PLING DATE: 1999-02-44
PRIOR PLING DATE: 1999-02-44
PRIOR PLING DATE: 1999-02-44
PRIOR PLING DATE: 1999-02-44
PRIOR PLING DATE: 1999-10-21
PRIOR PLING DATE: 1999-10-21
PRIOR PLING DATE: 1999-10-21
PRIOR PRIOR APPLICATION NUMBER: 09/1063,212
PRIOR PRING DATE: 1999-10-21
PRIOR PRING DATE: 1999-10-21
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Warsters, Scot A.
APPLICANT: Wood, William
TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P1206R1
CURRENT APPLICATION NUMBER: US/10/959,537
CURRENT FILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: 1998-02-09
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PRIOR PILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR PILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-15
PRIOR PILING DATE: 2001-11-15
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PRIOR PILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR PILING DATE: 2002-02-13
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PRIOR PILING DATE: 2002-02-13
PRIOR APPLICATION NUMBER: US 60/356,714
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PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR PILING DATE: 2002-02-13
PRIOR PILING DATE: 2002-02-13
PRIOR PILING DATE: 2002-02-13
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Best Local Similarity 100.0
Matches 241; Conservative
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US-10-295-027-1284
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US-10-959-537-3
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      APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TRI1, TRI1SVI,
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TRI1, TRI1SVI,
TITLE OF INVENTION: TRI1SV2
CURRENT APPLICATION NUMBER: US/10/27,966
CURRENT FILING DATE: 2000-10-23
PRIOR FILING DATE: 1099-02-23
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/144,076
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: 1999-10-21
PRIOR FILING DATE: 1998-10-21
PRIOR FILING DATE: 1998-10-21
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PRIOR PILING DATE: 1999-10-21
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APPLICANT: Aziz, Natasha
APPLICANT: Gish, Wurdy M.
APPLICANT: Gish, Rurt C.
APPLICANT: Gish, Rurt C.
APPLICANT: Hevezi, Peter A.
APPLICANT: Hevezi, Peter A.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Mack politions and TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer, CURRENT APPLICATION NUMBER: 102/10/295,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRD
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Publication No. US20030232350A1
GENERAL INFORMATION:
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Matches 241; Conservative
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ORGANISM: human
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; CRGANISM: Homo Sapiens
US-10-783-528-75
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US-10-783-528-75
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| Sequence 3, Application US/11032294
| Publication NO. US20050202008A1
| Publication NO. US20050202008A1
| GENERAL INFORMATION:
| APPLICANT: P. Mickey Williams
| APPLICANT: P. Mickey Williams
| APPLICANT: P. Mickey Williams
| TITLE OF INVENTION: CARDIOVASCULARIZATION OF ANGIOGENESIS AND
| TITLE OF INVENTION: LIGAND/RECEPTOR HOMOLOGS
| TITLE OF INVENTION: LIGAND/RECEPTOR HOMOLOGS
| TITLE OF INVENTION: LIGAND/RECEPTOR HOMOLOGS
| TITLE OF INVENTION: LIGAND/RECEPTOR HOMOLOGS
| CURRENT FILING DATE: 2005-01-10
| PRIOR PELLING DATE: CURRENT APPLICATION NUMBER: US/09/613,972
| PRIOR FILING DATE: 1999-07-12
| PRIOR FILING DATE: 1999-07-12
| NUMBER OF SEQ ID NOS: 22
| SEQ ID NOS: 22
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                                                                                                                                            DB 17; Length 241;
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                                                                                                                                        100.0%; Score 1386; DB 17;
100.0%; Pred. No. 1.1e-106;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 241; Conservative
                                                                                                                                                                               Matches 241; Conservative
        31
                                          LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-959-537-3
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ORGANISM: Homo sapiens
        NUMBER OF SEQ ID NOS:
SEQ ID NO 3
                                                                                                                                                             Best Local Similarity
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APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins
TITLE OF INVENTION: Human Tumor No 105, 593
CURRENT PERION NOWER: US/09/915, 593
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/121, 363
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/144,076
PRIOR FILING DATE: 1099-05-13
PRIOR FILING DATE: 1099-05-13
PRIOR FILING DATE: 1999-05-13
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1999-02-24
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Sequence 75, Application US/10783528
| Sequence 75, Application US/10783528
| Publication No. US20040219579A1
| GENERAL INFORMATION:
| APPLICANT: Aziz, Natasha
| APPLICANT: Gish, Kutt
| APPLICANT: Zlotnik, Albert
| TITLE OF INVENTION: METHIONS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND FILE REFERENCE: 05882.0191.NPUS01
| CURRENT APPLICATION NUMBER: US/10/783,528
| CURRENT FILING DATE: 2004-02-19
| NUMBER OF SEQ ID NOS: 116
| SOFTWARE: PATENTIN VERSION 3.2
| SEQ ID NO 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YPGEECCSEWDCMCVQPBFHCGDPCCTTCRHHPCPPGQCVQSQGKFSFGFQCIDCASGTF
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US-10-2//-966-2

Sequence 2, Application US/1027966

Sequence 2, Application US/1027966

Sequence 2, Application US/1027966

Sequence 2, Application NO. US20030153499A1

GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: Ni, Jian

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,

TITLE OF INVENTION: HUMBER: 2002-10-23

PRIOR APPLICATION NUMBER: 60/121,648

PRIOR PILING DATE: 1999-02-24

PRIOR APPLICATION NUMBER: 60/134,172

PRIOR APPLICATION NUMBER: 60/144,076

PRIOR PILING DATE: 1999-10-21

PRIOR PI
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                Score 1322.5; DB 14; Length 234; Pred. No. 1.9e-101; Mismatches 0; Indels 7;
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Best Local Similarity 96.7%; Pred. No. 1.9e-101;
Matches 233; Conservative 1; Mismatches 0;
                          95.4%;
                                                        Best Local Similarity 96.7
Matches 233; Conservative
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US-10-283-105-2

US-10-283-105-2

Sequence 2, Application US/10283105

Publication No. US2030138426A1

SEGURARAL PROPAMATION:

APPLICANT: Ni, Jian

APPLICANT: Nuben, Steven M

TITLE OF INVERTION: Human Thuror Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,

TITLE OF INVERTION: Human Thuror Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,

TITLE OF INVERTION: Human Thuror Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,

TITLE OF INVERTION: HUMBER: US/10/283,105

CURRENT APPLICATION NUMBER: 00/310,757

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-00-23

PRIOR PLING DATE: 2000-07-281

PRIOR APPLICATION NUMBER: 00/213,73

PRIOR APPLICATION NUMBER: 00/213,73

PRIOR APPLICATION NUMBER: 00/121,476

PRIOR APPLICATION NUMBER: 00/124,076

PRIOR PLING DATE: 1999-06-23

PRIOR PLING DATE: 1999-06-23

PRIOR PLING DATE: 1999-06-23

PRIOR PLING DATE: 1999-06-24

PRIOR PLING DATE: 1999-06-31

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Pred. No. 1.9e-101;
1; Mismatches 0;
## PRIOR FILING DATE: 1998-10-21
| PRIOR PELLING DATE: 1998-10-21
| PRIOR FILING DATE: 1997-10-21
| NUMBER OF SEQ ID NOS: 28
| SOFTWARE: Patentin Ver. 2.0
| LENGTH: 234
| TYPE: RRT
| TYPE: RRT
| ORGANISM: Homo sapiens
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Best Local Similarity 96.7%;
Matches 233; Conservative
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CRGANISM: human
US-10-283-105-2
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LENGTH: 234
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TSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
                         61 YPAQLLGGWPVSCPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSF 120
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Sequence 6, Application US/09915593

Sequence 10.25002009825A1

Sequence 6. Application US/09915593

Sequence 6. Application US/09915593

GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: Ni, Jian

APPLICANT: Ni, Jian

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins

TITLE OF INVENTION: Human Tumor Necrosis Factor

FILE REFRENCE: PF396P2

CURRENT APPLICATION NUMBER: US/09/915,593

CURRENT FILING DATE: 2000-07-27

PRIOR FILING DATE: 2000-07-28

PRIOR FILING DATE: 2000-07-28

PRIOR FILING DATE: 2000-02-23
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Publication No. US20040009491A1

GENERAL INFORMATION:

APPLICANT: Birse et al.

TITLE OF INVENTION:

CURRENT APPLICATION NUCLEIC Acids, Proteins, and Antibodies

FILE REFERENCE: PA131P1

CURRENT APPLICATION NUMBER: US/10/264,237

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR APPLICATION NUMBER: US 60/205,515

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

PRIOR FILING DATE: 2000-05-19

NUMBER OF SEQ ID NOS: 2876

SOFTWARE: PatentIn Ver. 3.1

LENGTH: 246
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94.3%; Score 1306.5; DB 1:
Best Local Similarity 92.1%; Pred. No. 4.3e-100;
Matches 233; Conservative 1; Mismatches 0;
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ORGANISM: Homo sapiens
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APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
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APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,
TITLE OF INVENTION: HUMBER: US/10/283,105
FILE REFERENCE: PF396P3
CURRENT PILING DATE: 2002-10-30
FRICR FILING DATE: 2001-10-30
FRICR FILING DATE: 2001-07-27
FRICR FILING DATE: 2001-07-27
FRICR FILING DATE: 2000-07-28
FRICR FILING DATE: 2000-07-28
FRICR FILING DATE: 2000-07-28
FRICR FILING DATE: 2000-07-28
FRICR FILING DATE: 1999-07-16
FRICR FILING DATE: 1999-07-16
FRICR FILING DATE: 1999-07-16
FRICR FILING DATE: 1999-07-16
FRICR FILING DATE: 1999-02-24
FRICR FILING DATE: 1999-02-24
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FRICR FILING DATE: 1999-02-24
FRICR FILING DATE: 1999-07-16
FRICR FILING DATE: 1999-02-24
FRICR FILING DATE: 1999-02-24
FRICR FILING DATE: 1999-010-21
FRICR FILING DATE: 1999-10-21
FRICR FILING DATE: 1999-10-21
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PRIOR FILING DATE: 2000-07-16
PRIOR PELING DATE: 2000-07-16
PRIOR APPLICATION NUMBER: 60/134,172
PRIOR PLING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: 60/121,648
PRIOR PILING DATE: 1999-02-24
PRIOR PILING DATE: 1999-102-24
PRIOR PILING DATE: 1999-10-21
PRIOR PILING DATE: 1998-10-21
PRIOR PILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-10-21
PRIOR FILING DATE: 1997-10-21
SEQ ID NO 6
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Publication No. US20030138426A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-09-915-593-6
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US-10-283-105-6
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completed: October 26, 2005, 16:11:21
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Job time: 116.618 secs
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Sequence 6, Application US/1027966

Publication No. US2030153499A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: Ruben, Steven

TITLE OF INVENTION: Humor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor-Like Proteins TR11, TR11SV1,

TITLE OF INVENTION: Humber: US/10/277,966

CURRENT PELING DATE: 2002-10-23

PRIOR APPLICATION NUMBER: 09/512,363

PRIOR APPLICATION NUMBER: 60/121,648

PRIOR FILING DATE: 1999-02-24

PRIOR FILING DATE: 1999-05-13

PRIOR PRILING DATE: 1999-07-16

PRIOR PRILING DATE: 1999-10-21

PRIOR PRILING DATE: 1997-10-21

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GGWPVSCPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVGSQGKFSFGFQCID 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 ACVLLITSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKG 234
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Pred. No. 1.9e-97;
1; Mismatches 0; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                7 MGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDY----
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                             Query Match 92.0%; Score 1274.5; DB 14; Length 240; Best Local Similarity 91.9%; Pred. No. 1.9e-97; Matches 227; Conservative 1; Mismatches 0; Indels 19;
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: human
US-10-283-105-6
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91.9%;
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Best Local Similarity 91.9
Matches 227; Conservative
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US-10-277-966-6
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US-10-277-966-6
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175 ACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKG 234
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------ PGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCID 114
                                                                                         CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 26, 2005, 15:38:30 ; Search time 25.693 Seconds (without alignments) 902.513 Million cell updates/sec

US-09-545-998B-4 1386 1 MAQHGAMGAFRALCGLALLC......EEERGERSAEEKGRLGDLWV 241 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	T-cell antigen 4-1	ocyte		OX40 antigen precu	OX40 homolog - hum	B cell-associated	D)	laminin beta-2 cha		death receptor-6 -	tumor necrosis fac		B-cell activation	ε		laminin beta-2 cha	laminin alpha 5 ch	laminin beta-2 cha	EGF repeat transme			hypothetical prote	hypothetical prote	notch 3 protein -	fibrillin-2 precur	protein T22F7.3 [i	hypothetical prote		apolipoprotein E r
ΩI	B32393	138426	148700	S12783	137552	A46476	JC5559	MMRTS	154182	JC7705	A35356	T13954	A60771	I48854	B38634	853869	T10053	A55677	T30176	A33837	A48805	T18975	T26972	S45306	A57278	H88380	T24272	A46019	JE0237
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Length	256	255	272	271	277	305	295	1801	435	651	461	1574	277	459	474	1798	3635	1797	1687	1371	329	152	1111	2318	2907	1522	164	2531	966
% Query Match	14.2	14.1	12.6	12.2	11.7	10.4	10.0	9.7	9.6	9.4	9.3	9.5	8.9	8.8	8.7	8.6	8.6	8.5	8	8.3	8.3	8.1	8.0	8.0	0.8	7.9	7.9	7.9	7.9
Score	197	195.5	175	168.5	162	144.5	139	134.5	133	130.5	129	127.5	124	121.5	121	119.5	119	118.5	117.5	115.5	114.5	112	111	111	110.5	110	109.5	109.5	109
Result No.	1	N	٣	4	ß	9	7	α ο	Ø.	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

RESULT 2

insulin receptor-r	ribrillin-2 precur	hypornerical proce	low-density lipopr	latent transformin	hypothetical prote	thrombospondin 2 p	tenascin-X precurs	Doc4 protein, stre	MEGF8 protein - hu	LDL receptor relat	LDL receptor-relat	thrombospondin 3 -	agglutinin isolect	MEGF2 protein - hu	fibrillin I - bovi
B47417	A54105	T25061	JE0315	A57293	T15651	TSHUP2	A40701	T14271	T00209	T00204	T00203	A46016	A28401	T00250	A55567
7	~	~	~	N	~	-	-	~	0	~	7	-	~	~	0
540	2918	788	1113	1251	188	1172	3566	2825	1737	770	770	926	186	1364	2871
7.8	7.7	7.6	7.6	7.6	7.6	7.6	7.6	7.5	7.5	7.4	7.4	7.4	7.4	7.4	7.4
108	106.5	106	105.5	105.5	105	105	105	104.5	103.5	102.5	102.5	102.5	102	102	102
30	31	32	33	34	35	36	37	38	36	4	41	42	43	44	45

ALIGNMENTS

us-09-545-998b-4.rpr

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Local Similarity
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A; Residues: 1-271 < MAL>
A; Accession: I48334
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Matches
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A; Residues: 1-106, 'R', 108-255 sSCH>
A; Residues: 1-106, 'R', 108-255 sSCH>
A; Residues: 1-106, 'R', 108-255 sSCH>
A; Residues: 1-106, 'R', 108-255 sSCH>
C; Comment: This protein belongs to a member of the human nerve-growth-factor/tumor-necro C; Comment: This protein belongs soluble, call-surface bound or extracellular matrix C; Superfamily: CD27 antigen; MSF receptor; transmembrane protein
F; Superfamily: CD27 antigen; MSF receptor; transmembrane protein
F; 1-17/Domain: signal sequence #status predicted <SIG>
F; 1-17/Domain: transmembrane #status predicted <TMN>
F; 187-213/Domain: transmembrane #status predicted <TMN>
F; 138, 149/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 242/Binding site: phosphate (Thr) (covalent) (by protein kinase I) #status predicted
F; 242/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
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N;Alternate names: OX40 antigen
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 148700; 148334; $34377
R;Calderhead, D.M.; Bublimann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
A;Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell int
A;Reference number: 148700; MUID:94044750; PMID:8228223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: UNIPROT: P47741; EMBL: Z21674; NID: 9312827; PIDN: CAA79772.1; PID: 93128
Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-255 <RES,
A;Cross-references: UNIPROT:Q07011; EMBL:U03397; NID:g571320; PIDN:AAA53133.1; PID:g5713
R;Schwarz, H.; Tuckwell, J.; Lotz, M.
Gene 134, 295-298, 1993
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                                                                                                                                                           В.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Title: A receptor induced by lymphocyte activation (ILA): a new member of the human A,Reference number: JT0752; MUID:94085794; PMID:8262389
                                                       C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 138426; JT052
R;Alderson, M.R.; Smith, C.A.; Tough, T.W.; Davis-Smith, T.; Armitage, R.J.; Falk,
Eur. J. Immunol. 24, 2219-2227, 1994
A;Title: Molscular and biological characterization of human 4-18B and its ligand.
A;Reference number: 138426; MUID:94374434; PMID:8088337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 150 GTKERDVVCGPSPADLSPGASSVTPPAPAREPGHSPQIISFFLALTSTALLFFLFFLTFL 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNKTHNAVCVPG-----SPPA---EPLGWLTVV--LLAVAACVLLLTSAQLGLH 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48 CPPNSFSSAGG--ORTCDI-----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS-----EWDCMCVQPEFHCGDP
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                                lymphocyte activation-induced receptor ILA precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.1%; Score 195.5; DB 2; 28.8%; Pred. No. 3.8e-08; tive 21; Mismatches 81;
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A;Molecule type: mRNA
A;Residues: 1-272 <RES>
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66; Conservative
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A; Status: translated
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OX40 antigen precursor - rat
NiAlternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S12783; S08036
R;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes
A;Reference number: S12783; MUID:90214614; PMID:2157591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:P15725; EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831; Superfamily: CD27 antigen; NGF receptor repeat homology; Keywords: growth factor receptor; transmembrane protein; 1-19/Domain: signal sequence #status predicted <SIG> 1-19/Domain: signal sequence #status predicted <ARG> 1-10/Domain: transmembrane #status predicted <ARG> 211-235/Domain: transmembrane #status predicted <ARM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PCPPGQGVQSQGKFSF 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----CPPGQGVQSQGKFSFGFQCID 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 GEYNEAVNYDICKOCIOCHHRSGSELKONCIPIODIVCRCRPGIQPRODSGYKLGVDCVP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 CASGIFSGGHEGHCKPWIDCIQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 GFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- 167
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A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-14, G', 16-272 <RE2>
A;Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C;Genetics:
A;Gene: ox40
A;Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C;Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 LLLGTGTDAR--CCRVHT----TRCCRD-YPG----EECCSEWDCMCVQPEFHCGDPC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 LALTLGVTARRINCVKHTYPSGHKCCRECOPGHGMVSRCDHTRDTLC------HPCET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 QQPT-----AFLILGLSLGVTVKLNCVKDTYPSGHKCCRECQPGHGMVSRCDHTRDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 CHPCEPGFYNEAVNYDTCKQCTQCNHRSGSELKQNCTPTEDTVCQCRPGTQPRQDSSHKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 ORPIGGPGCGPGRLLLG--TGTDARCCRVHTT-----RCCRD-YPGEECCSEWD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                           70;
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                                                                                                                                                                                                                                                                                                                         Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 GVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDTVCEDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 VLLAVAACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPST 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 -LLA----TLLWETQRTTFRPTTVPSTTVWPRTSQL----PST 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80;
                                                                                                                                                                                                                                                                                                                     Query Match
12.6%; Score 175; DB 2; I
Best Local Similarity 26.7%; Pred. No. 1.6e-06;
Matches 58; Conservative 19; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.2%; Score 168.5; DB 2 27.7%; Pred. No. 4.9e-06; Live 17; Mismatches 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 ACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 CMCVQPEFHCG----DPC--CTTCRHH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 -----CTTCRHHP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62; Conservative
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C,Accession: S03539
R;Hunter, D.D.; Shah, V.; Merlie, J.P.; Sanes, J.R.
Nature 338, 229-234, 1989
A;Tile: A laminin-like adhesive protein concentrated in the synaptic cleft of the neuron A;Reference number: S03539; MUID:89159410; PMID:2922051
A;Accession: S03539.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1801 <HUN>
A;Cross-references: UNIPROT:P15800; EMBL:X16563; NID:g57250; PIDN:CAA34561.1; PID:g57251
C;Complex: Laminins are trimers of an alpha-type, a beta-type, and a gamma-type laminin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Accession: JC5559
R;Yamaguchi, K.; Yurino, N.; Kino, M.; Ishiguro, M.; Funatsu, G.
Biosci. Biotechnol. Biochem. 61, 690-698, 1997
A;Title: The amino acid sequence of mitogenic lectin-B from the roots of pokeweed (Phytol A;Reference number: JC5559; MUID:97290889; PMID:9145528
A;Reference number: JC5559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Experimental source: root
C, Comment: This protein is a lectin specific for N-acetylgucosamine-containing saccharide
C, Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; ple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 SEWDCMCVQPEFHCGDPCCTTCRHHPCPPGGGVQSQGKFSFGFQ-C---IDCASGTFSGG 123
                                                                                                                                                                                                                 145
                                                                                                                                                                                                                                                                         119 CAQHTPCIPGFGVMEMATETTDTVCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKG 178
                                                                                                                                                                                                                                                                                                                                                                                                 179 TSQTNVICGLKSR-----PKALLVIPVVMGILITIFGVFLYİKKVVKK---PKDNEML 228
                                                                                                                                              59 CHPCDSGEFSAQWNREIRCHQHRHCEPNQGLRVKKEGTAESDTVCTCKEGQHCTSKDCEA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Phytolacca americana (Virginian pokeweed)
C;Dite: 02-Sep-1997 #sequence_revision 05-Sep-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laminin beta-2 chain precursor - rat
N'Alternate names: laminin chain B3: S-laminin
C:Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 CALSLGQRPTGGP-----GCGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECC
---RVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT
                                                                                                                                                                                                              89 C-RHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGHE--GHCKPWTDCTQFGFLTVFPG
                                                                                                                                                                                                                                                                                                                                            146 NKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQLRSQCMWPRETQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Keywords: glycoprotein F;96,139/\mathrm{Binding} site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30;
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; Pred. No. 0.001;
18; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | : | | : | | : | | --- pPAARRQDPQEMEDYPGHNTAAPVQETLHGCQPVTQEDGKES 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: UNIPROT: Q9AVB0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.8%;
Matches 36; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lectin-B - Virginian pokeweed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 1-295 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 LEVPPST---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46476; A46515
Forres, R. M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine
A;Reference number: A46476; MUID:92105763; PMID:1370315
                                                                  C; Species: Homo sapiens (man)
C; Date: 29-May-1998 #text_change 09-Jul-2004
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C; Accession: 137552
R; Latza, U.; Durkop, H.; Schnittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fonat Eur. J. Immunol. 24, 677-683, 1994
A; Title: The human OX40 homolog: CDNA structure, expression and chromosomal assignment characterice number: 137552; MUID: 94170844; PMID: 7510240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-305 < TORS
A; Residues: 1-305 < TORS
A; Cross = references: UNIPROT: P27512; GB: M83312; NID: 91553058
A; Cross = references: UNIPROT: P27512; GB: M83312; NID: 91553058
A; Note: sequence extracted from NCBI backbone (NCBIN: 75206, NCBID: 75207)
A; Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
B; Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J. Immunol. 149, 3921-3926, 1992
A; Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A; Reference number: A46515; MUID: 93094586; PMID: 1281194
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: UNIPROT:P43489; EMBL:X75962; NID:9472957; PIDN:CAA53576.1; PID:94729 Superfamily: CD27 antigen; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 17-287, LVV <cRI>A;Residues: 17-287, LVV <cRI>A;Cross-references: GB:MB3312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; A;Cross-references: GB:MB3312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; A;Cross-references: BALB/C, liver A; DackDone (NCBIP:120357) C;Comment: For an alternative splice form, see PIR:A46515. C;Comment: For an alternative splice form, see PIR:A46476. C;Superfamily: CD27 antigen; NGF receptor repeat homology C;Reywords: alternative splicing; transmembrane protein F;105-144/Domain: NGF receptor repeat homology <NGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 TRCCRDYPG--EECCSEWDCM-CVQPEFHCGD---PCCTTCRHHPCPPGQGVQSQGKFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 GAMGAFRALCGLALLCALSLG------QRPTGGPGCGPGRLLLGTGTDARCCRVHT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.4%; Score 144.5; DB 2;
llarity 22.8%; Pred. No. 0.00039;
Conservative 27; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.7%; Score 162; DB 2;
29.7%; Pred. No. 1.6e-05;
:ive 11; Mismatches 92
                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-277 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 29.7%
nes 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 65; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: A46476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 65
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Matches
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Gaps

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171 232

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NyAlternate names: 75K tumor necrosis factor receptor; TNF receptor type 2 C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text change 09-Jul-2004 C; Accession: A35356; A36475; A48416; A36007; A23666; B335010; I38094 R; Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C, Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-651 <BRI>
A;Cross-references: UNIPROT:Q98SM6; GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
tresia, activates a cell death and/or survival signaling cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fil21/Domain: signal sequence #status predicted <SIG>
Fi22-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
Fi322-250/Domain: transmembrane #status predicted <TVM>
Fi310-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 RCHPCRKPCELPMIEKTHC-----TALIDRECTCLSGTFQINDICVP---YTVCPVGW 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 GVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPGNKTHNAVCVPG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 GVRKKGTETEDVRCKPCLRGTFSDVPSSVMKCKTYTDCFGKNMVVVKPGTKESDNVC--X 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Species: Gallus gallus (chicken)
C,Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: JC7705

R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.

Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001

A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.

A;Reference number: JC7705; MUID:21308433; PMID:11414698
                                                                                                                                                                                                                                                                                  62 CPP----GTYVSAKCSRIRDTVCATCAENSYNEHWNYLTICOLCRPCDPVMGLEBIAPC
                                                                                                                                                                                                                                                                                                                                                                  67 CS--EWDCMCVQPEFHCGDPC--CTTCR-HHPCPPGQGVQSQGKFSFG-FQCIDCASGTF
                                                                                                                                                                                                                                                                                                                                                                                                                   117 TSKRKTQCRC-QPGMFCAAWALECTHCELLSDCPPGTEAELKDEVGKGNNHCVPCKAGHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLG------WLTVVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 QNTSSPSARCQPHTRCENQGLVEAAPGTAQSDTTC---KNPLEPLPPEMSGTMLMLAVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 RC--CR-----VHTTRCCRDYPGEECCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 PLAFFLLLATV-----FSCIWKSHPSLCRKLGSLLKRPOGE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 AVAACVLLITSAQLGLHIWQLRSQCMWPRETQL-----LLEVPPSTE 213
                                                    DB 2; Length 435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length
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                                                                                                                            86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.4%; Score 130.5; DB 29.8%; Pred. No. 0.0084;
                                                Query Match 9.6%; Score 133; DB 2
Best Local Similarity 25.0%; Pred. No. 0.004;
Matches 57; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                             34 CGPGRLLLGTGTDARCCRVHTTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      death receptor-6 - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         198 SPASLPNTSLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
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A35356
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C; Function:
A; Description: interact with cells and with other basement membrane proteins to promote A; Description: interact with cells and with other basement membrane predicts of Step. 118 homology
C; Seywords: basement membrane; calcium binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cell binding; cel
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-435 <RES>
A,Cross-references: UNIPROT:P36941; GB:L04270; NID:g339761; PIDN:AAA36757.1; PID:g339762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nap position: 12p13.3-12p13.1
Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: 154182
R;Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Rsaens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
A;Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequent A;Reference number: 154182; MUID:93252381; PMID:8486360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;45-50/Disulfide bonds: #status predicted
F;251,371,1088,1252,1311,1351,1502/Binding site: carbohydrate (Asn) (covalent) #status
F;1193,1196,1800/Disulfide bonds: interchain #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 944 TSCHRDGYSQQIVCHCRAGYTGLRCEACAPGHFGDPSKPGGRCQLCECSGNIDPTDPGAC 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          840 GALSALCEGTSGQCLCRTGAFGLRCDHCQRGQWGFPNCRPCVCNGR-----ADECDA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 HTTRC--CRDYPGEECCSEWDCMCVQPEFHCGDPCCT---TCRHHPCPPGQGVQSQGKFS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
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.Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 GAFRALC-GLALLCALSLG-----QRPTGG-PGCGP----GRLLLGTGTDARCCRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    892 HTGACLGCRDYTGGEHCER----CI-AGFH-GDPRLPYGGQCRPCPCPEGPG--SQRHFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-VPGSPP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.7%; Score 134.5; DB 1; Length 1801;
26.9%; Pred. No. 0.0088;
tive 6; Mismatches 60; Indels 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumor necrosis factor receptor 2-related protein - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB: LTBR
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                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 63; Conserv
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                                                                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Rossiduss: 1-461 <SMI>
A;Coss-references: UNIPROT:P20333; GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
A;Cross-references: UNIPROT:Paker, S.L.; Schwartz, P.B.; King, M.W.; Hale, K.K.; Squires,
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A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
A;Reference number: A36475; MUID:91045991; PMID:2172983
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A;Status: preliminary
A;Nolecule type: mRNA; protein
A;Residues: 23-461 «DEMA
A;Cross-references: GB:S63368; NID:9235648; PIDN:AAB19824.1; PID:9235649
A;Cross-references: GB:S63368; NID:9235648; PIDN:AAB19824.1; PID:9235649
A;Cross-reference extracted from NCBI backbone (NCBIN:63368, NCBIP:63371)
B;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra A;Reference number: A36007; WUID:90349572; PMID:2166946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homold C;Keywords: duplication; glycoprotein; receptor; transmembrane protein F;1-22/Domain: signal sequence #status predicted <SIG> F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 116-140, 'P',142-195,'R',197-362,'T',364-461 <HEL>
A;Cross.references: GB:M35857; MID:g339751; PIDN:AAA63262.1; PID:g339752
R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
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A;Title: Purification and partial amino acid sequence analysis of two distinct tumor ned
A;Reference number: A23666; MUID:91056048; PMID:2173696
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A;Molecule type: protein
A;Molecule 13-40(65-69)136-141;300-306 <LOE>
A;Residues: 23-40(65-69)136-141;300-306 <LOE>
A;Residuenn, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
J. Biol. Chem. 265, 1531-1536, 1990
J. Biol. Chem. 265, 1531-1536, 1990
A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A;Reference number: A35010; MUID:90110215; PMID:2153136
A;Accession: B35010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-195,'R', 197-461 <KOH>
A; Residues: 1-195,'R', 197-461 <KOH>
A; Cross-references: GB MS5994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
R; Dembic. Z; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.
Cytokine 2, 231-237, 1990
A; Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
A; Reference number: A48416; MUID:91370690; PMID:1966549
Science 248, 1019-1023, 1990
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
A;Reference number: A35356; MUID:90260639; PMID:2160731
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Gene 150, 381-386, 1994
A;Title: Cloning, sequencing and partial functional cha.
A;Reference number: 138094; MUID:95121934; PMID:7821811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-37 <RES>
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A.Cross-references: UNIPROT:088281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g34
A.Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEGF6 protein - rat
C;Species: Rattus norvėgicus (Norway rat)
C;Species: Co-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs A;Reference number: 214126; MUID:98360089; PMID:9693030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96 PGQGVQSQGKFSFGFQCIDCASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVP 155
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                                                                                                                                                                                                                                                                                                                                                                                           72 -CMCVQPEFHC-----GDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSG--
                                                                                                                                                                                                                                                                                                                                    57 CSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSRCSSDQVETQACTREQNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC-----VPG-----VPG-----
                                                                                                                                                                                                                                                                                34 CGPG---RLLLGTGTDARC------CRVHTTRCCRDYPGEECCSEWD--
F;120-162/Domain: NGF receptor repeat homology <NG3>
F;164-201/Domain: NGF receptor repeat homology <NG4>
F;262-279/Domain: transmembrane #status predicted <TMN>
F;280-461/Domain: intracelular #status predicted <INT>
F;11,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61;
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                                                                                                                                                                     9.3%; Score 129; DB 1; Length 461;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                            27; Mismatches
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165

210

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A;Accession: S54816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <KIS>
A;Cross-references: EWBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
C;Keywords: cytokine receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-74/#product: tumor necrosis factor receptor type 2 #status predicted <MAT>
F;40-77/Domain: NGF receptor repeat homology <NG3>
F;79-120/Domain: NGF receptor repeat homology <NG3>
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A;Residues: 1-474 <LEM>
A;Residues: 1-474 <LEM>
A;Cross-references: UNIPROT:P25119; GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828

R;Goodwin, R.G; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenkj
MOI. Cell. Biol. 11, 3020-3026, 1991
A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for t
A;Reference number: A40254; MUID:91246168; PMID:1645445
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C;Accession: B38634; A40254; $\overline{5}\)54816
C;Accession: B38634; A40254; $\overline{5}\)54816
F;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, B.Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
A;Title: Cloning and expression of CDNAs for two distinct murine tumor necrosis factor A;Reference number: A38634; MUID:91187885; PMID:1849278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
R;Kissonerghis, M.; Fellowes, R.; Fellowes, R.; Fellowes, R.; Fellowes, R.; Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowes, Fellowe
                                                                                                                                                                    Indels 101; Gaps 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 EIRACTKQQNRVCACEAGRYCAL-----KTHSGS--CRQCMRLSKCGPGFGVASSR 155
                                                                                                                                                                                                                                                                                                                                                                                                                                             RTCLSCSSSCSTDQVETRACTKQQNRVCACEAGRYCALKTHSGS--CRQCMRLSKCGPGF 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 GVASSRAPNGNVLCKACAPGTFSDTTSSTDVCRPHRICS----ILAIPGNASTDAVCAPE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              191 SPILSAIPRILYVSQPEPTRSQPLDQEPGPSQTPSILTSLGSTPIIEQSTKGGISLPIGL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 IVGVTSLGLLMLGLVNCFILVQRKKKFSCLQRDAKVPHVPDEKSQDAVGLEQQHLLTTAP 310
                                                                                                                                                                                                                                                                                                            48 RCCRVHTTRCCRDYPGEECCSEWD---CMCVQPEF----HCGDPCCTTC-RHHPCPPGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVQSQGKFSFGFQCIDCASGTFSG--GHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LIVVLLAVAACVLLLTSAQLGL-----HIWQLRSQCMWPRETQLLLEVPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.7%; Score 121; DB 2; Length 474;
ilarity 21.1%; Pred. No. 0.036;
Conservative 27; Mismatches 92; Indels 102;
                            Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STE------DARS----CQFPEERGERSAEEKGRLGD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |: | : | : | : | SSSSSSLESSASAGDRRAPPGHPQARVMAEAQGSQEARASSRISD 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor necrosis factor receptor type 2 precursor - mouse C; Species: Mus musculus (house mouse)
                            Query Match 8.8%; Score 121.5; DB 2; Best Local Similarity 21.0%; Pred. No. 0.032; Matches 60; Conservative 29; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;166-203/Domain: NGF receptor repeat homology <NG4>
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Matches 59; Conserv
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A; Residues: 1-474 <GOO>
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C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homold
F;151-188/Domain: NGF receptor repeat homology <NGF>
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A; Map position: 20q12-20q13.2
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Superfamily: CD27 antigen; NGF receptor repeat homology
C; Superfamily: CD27 antigen; NGF receptor repeat homology
E; 1-2070 Domain: signal sequence #status predicted <SIG>
E; 21-277 Product: B-cell activation protein CD40 #status experimental <MAT>
F; 21-277 Product: B-cell activation protein CD40 #status experimental <MAT>
F; 21-277 Pomain: extracellular #status predicted <PRM>
F; 216-277 Pomain: intracellular #status predicted <CYT>
F; 216-277 Pomain: intracellular #status predicted <CYT>
F; 216-277 Pomain: intracellular #status predicted <CYT>
F; 216-277 Pomain: intracellular #status predicted <PRM>
F; 216-277 Pomain: intracellular #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-277 <5Th,
A; Residues: 1-277 <5Th,
A; Cross-treferences: UNIPROT: P25942; EMBL: X60592; NID: G29850; PIDN: CAA43045.1; PID: G29851
R; Braesch, Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
J. Immunol. 142, 562-567, 1989
A; Title: Biochemical characteristics and partial amino acid sequence of the receptor-lik
A; Reference number: A60771; MUID: 89093941; PMID: 2463309
B-cell activation protein CD40 precursor - human NyAlternate names: B-cell surface antigen BD50 (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: O3-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004 (Spacession: 804460, A6071) (Spacession: 504460, A6071) (Spacession: A1403-1410, 1993 #sequence_revision molecule related to the nerve growth factor receptor A; Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor A; Reference number: 804460; MUID:89356608; PMID:2475341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 TNKTDVVC----GPODRLRALVVIPIIFGILFAILLVLVFIKKVAKKPTNKAPHPKOEPO 234
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C;Species: Mus musculus (house mouse)
C;Date: 02-011-1996 #sequence_revision 02-011-1996 #text_change 09-011-2004
C;Accession: 148854
R;Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome S, 726-727, 1994
A;Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A;Reference number: 148854; MUID:95178848; PMID:7873884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C-RHHPCPPGOGVQSQGKFSFGFQCIDCASGTFSGGHEG--HCKPWTDCTQFGFLTVFPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG----EECCSEWDCMCVQPE-FHCGDPCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 21-50 <BRA>
A;Experimental source: Burkitt lymphoma cell line Raji
C;Genetics:
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A;Molecule 'type: mannA
A;Residues: 1-459 <RESA
A;Cross-references: UNIPROT:Q62327; EMBL:X76401; NII
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Query Match Best_Loc Matches 11;

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Search completed: October 26, 2005, 15:52:34 Job time : 26.693 secs

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US-09-545-998B-4 1386 1 MAQHGAMGAFRALCGLALLC......EEERGERSAEEKGRLGDLWV 241 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched: 1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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d	Query Match	100.0	53.1	53.1	14.6	14.5	14.2	14.1	13.8	13.2	13.1	12.8	12.6	12.6	12.3	12.3	12.2	11.7	11.4	11.0	10.8	10.7	10.5	10.4	10.4	10.4	10.4	10.2	10.2	10.2		10.1
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ALIGNMENTS

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CYCOPIONIC (Potential).
TNFR-Cys 1.
TNFR-Cys 2.
TNFR-Cys 3.
TNFR-Cys 3.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAc. . .) (Potential).
TQFGFLTVFPGNKTHNAVCVPGSPPAEPLGMLTVVLLAVAA CVLLITSAQLGLHIWQLRSQCWWPRETQLLLEVPEPTEDAR SCQPPEEERGERSAEEKGRLGDLWV -> CWRCRRRPKTPE
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                                                                                                                                                                                                                                                                                                                     Name=2; Synonyms=GITR-D;
IsoId=09Y5U5-2; Sequence=VSP 006508;
IsoId=09Y5U5-2; Sequence=VSP 006508;
IsoId=0PECIFICITY: Expressed in lymph node, peripheral blood leukocytes and weakly in spleen.
-!- INDUCTION: Up-regulated in peripherical mononuclear cells after antigen stimulation/lymphocyte activation.
-!- SIMILARITY: Contains 3 TNFR-Cys repeats.
                         "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
                                                                                                                         "Signal peptide prediction based on analysis of experimentally verified cleavage sites.";
Protein Sci. 13:2819-2824 (2004).
-:- FUNCTION: Receptor for TMFSTB. Seems to be involved in interactions between activated T lymphocytes and endothelial and in the regulation of T cell receptor-mediated cell death.
Mediated NF-kappa-B activation via the TRAFZ/NIK pathway.
-:- SUBUNIT: Binds to TRAFI, TRAFZ, and TRAFZ) but not TRAFS and
S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS. GO:0005916; P:anti-apoptosis; TAS. GO; GO:0005916; P:signal transduction; TAS. InterPro; IPR01368; TNRR c6. PROSITE; PS00652; TNRR NGFR 1; FALSE.NEG. PROSITE; PS00650; TNRR NGFR 1; FALSE.NEG. Alternative splicing; Direct protein sequencing; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
                                                                                                   PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally
                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane protein (isoform 1).
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                                                  bioinformatics assessment.";
Genome Res. 13:2265-2270(2003)
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241
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              Gray A.;
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                                            GAPQAAGALKSALGRALLPWQQKWVQEGGSDQRPGPCSSAA
AAGPCRRERETQSWPPSSLAGPDGVGS (in isoform
AASSPRKSGASDRQRRRGGWETCGCEPGRPPGPPTAASPSP
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the tumor necrosis factor/nerve growth factor receptor family.";
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MEDLINE=20292073; PubMed=10836847;
Mocentini G., Ronchetti S., Bartoli A., Spinicelli S., Delfino D.,
Brunetti L., Migliorati G., Riccardi C.;
"Identification of three novel mRNA splice variants of GITR.";
cell Death Differ. 7:408-410(2000).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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MEDLINE=20256302; PubMed=10798444; DOI=10.1089/104454900314474;
Nocentini G., Bartoli A., Ronchetti S., Giunchi L., Cupelli A.,
Delfino D., Migliorati G., Riccardi C.;
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SQCMWPRE -> K (in Ref. 2)
90DC3B4AA7E82CBE CRC64;
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035714; O9JKR1; O9JKR3; O5JKR3;
16-OCT-2001 (Rel. 40, Created)
15-OCT-2001 (Rel. 40, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 18 in a construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the construction of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAQHGAMGAFRALCGLALLCALSLGQRPTGGPGCGPGRLLL
                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 1386; DB 1;
; Pred. No. 9.9e-110;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FROM N.A. (ISOFORMS B; C AND D)
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                                                                                                                                                                                                                                                                                                                              26000 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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SEQUENCE FROM N.A. (ISOFORM A).

SEQUENCE FROM N.A. (ISOFORM A).

SEQUENCE SEQUENCE FROM N.A. (ISOFORM A).

STRAIN=C57BL/63; TISSUE=Thymus;

RA MEDIN=C257BL/63; TISSUE=Thymus;

RA MEDIN=C257BL/63; TISSUE=Thymus;

RA MIXAID E-2456681; DOI=10.1038/nature01266;

RA ASIAR Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA ABIAR Y., Furuno M., Basito R., Schonbach C., Gojobori T.,

RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P., Bult C.F., Hume D.A., Quackenbush J.,

RA Baldarelli R., Martagada H., Batalov S., Beisel K.W.,

RA Gasterland T., Gariboldi M., Gissi C., Gofazik A., Gough J.,

RA Anai A., Kawaji H., Kawasawa Y., Nedaierski R.M., King B.L.,

RAnai A., Kawaji H., Kawasawa Y., Lee Y., Lenhard B., Lyons P.A.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

RA Maquebina T., Mumata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.L., Miki H.,

RA Sandelin A., Schneider C., Semple C.A., Sercu M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Sercu M., Shimada K.,

Sandelin A., Schneider C., Semple C.A., Wang Y., Wang I., Yang I.,

Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Sakazume N., Sato K.,

RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Arasada T., Koman T., Koman Y., Aizawa M., Sakaik W., Sakaik W., Shibata K., Shinagawa A.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakaika M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sakaik M., Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SUBUNIT: Binds to TRAF1, TRAF2, and TRAF3, but not TRAF5 and TRAF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (By similarity).

**SUBCELLULAR LOCATION: Type I membrane protein (isoforms A, B and C); secreted (isoform D).

**ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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--- FUNCTION: Receptor for TNFSF18. Seems to be involved in interactions between activated T lymphocytes and endothelial cells and in the regulation of T cell receptor-mediated cell death. Mediated NF-kappa-B activation via the TRAF2/NIK pathway (By

IsoId=035714-2; Sequence=VSP_006510; IsoId=035714-1; Sequence=Displayed;

'n

Isold=035714-4; Sequence=VSP_006509; TISSUE SPECIFICITY: Preferentially expressed in activated T lymphocytes.

IsoId=035714-3; Sequence=VSP_006511;

Name=D;

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). -!- INDUCTION: Up-regulated in peripherical mononuclear cells after antigen stimulation/lymphocyte activation.

EMBL; AF109216; AAF14231.1; -. EMBL; AF229432; AAF61566.1; -. EMBL; AF229433; AAF61567.1; -. EMBL; AF204344; AAF61568.1; -. EMBL; AK020762; BAC25639.1; -. EMBL; U82534; AAB81243.1; -. MGD; MGI:894675; Infrsf18.

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66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65
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                                                                                                                                                                                                                                                      N-linked (GlCNAC. .) (Potential).
NCSOPGFLTMFPGNKTHNAVCIPEPLPTEQYGHLTVIFLVM
AACIFFLTTVQLGLHIWQLRRQHMCPRETQPFAEVQLSAED
                                                                                                                                                                                                                                                                                                                            -> VILORPSHSRRCSCOLRMIAASSSLRRNAGSROKKSVI
WGVGGHEAWSSSVPQARRYKTCPAIPLVRAGAMLCTLPWAW
PCSPQQWRKWVYESGELRLGPWAAFLI (in isoform
                                                                                                                                                                                                                                                                                     ACSFQFPEEERGEQTEEKCHLGGRWP -> KDPAIRGGAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE
                                                                                                                                                                                                                                                                                                                                                                               ETOPFAEVOĽSAEDACSFOFPEEERGEOTEEKCHLGGRWP
-> GOLCPREGENVSQAPHLPOFYYRDPAIRGGAVVS (in
                                                                                                                                                                                                                                                                                                                   ETQPFAEVQLSAEDACSFQFPEEBRGEQTEEKCHLGGRWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                              (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                           53.1%; Score 735.5; DB 1; Length 228; 57.0%; Pred. No. 1.6e-54;
        InterPro; IPR001368; TNFR_c6.
SMART; SM00181; EGF; 1.
SMART; SM00208; TNFR; 2.
PROSITE; PS00552; TNFR, 1; FALSE_NEG.
PROSITE; PS00552; TNFR NGFR_1; FALSE_NEG.
Alternative splicing; Ğlycoprotein; Receptor; Repeat; Signal;
                                                                                       Tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                          Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                               FTId=VSP_006511.
50D8C275D9C56259 CRC64;
                                                                                                                               Cytoplasmic (Potential).
                                                                                                                                                                                                                                               (GlcNAc. . .)
                                                                                                 superfamily member 18.
                                                                                                                                                                     By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAc...)
                                                                                                                                                                                                                                                                                                                                                                      FTIG=VSP 006510
                                                                                                                                                                                                                                                                                                 S (in isoform D)
/FTId=VSP 006509
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                                                                                                                                                   TNFR-Cys 2.
TNFR-Cys 3.
                                                                                                                                                                                                                                                                                                                                                                                                     isoform C)
                                                                               Potential
                                                                                                                       Potential
                                                                                                                                                                                                                                                                                                                                                                                                                          228 AA; 25334 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 134; Conservative
InterPro; IPR006210; IEGF
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142
444
744
744
122
36
121
121
131
134
134
134
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                                                                                                                                                                                                                                                                                                                                                                                  189
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1154
1754
175
28
62
62
62
63
1103
36
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                                                                     Transmembrane
                                                                                                           DOMAIN
TRANSMEM
DOMAIN
REPEAT
REPEAT
REPEAT
DISULFID
                                                                                                                                                                                                                           CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                        CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                 DISULFID
                                                                                 SIGNAL
                                                                                          CHAIN
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126 GHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQL 186 GLHIWOLRSOCMWPRETQLLLEVPPSTEDARSCOFPEERGERSAEEKGRLGDLW 240 Q8C4K3 PRELIMINARY; PRT; 250 AA.
Q8C4K3, Q6C4K3 (GC4K2)
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMSLrel. 26, Last annotation update)
Mus musculus 16 days embryo head cDNA, RiKEN full-length enriched library, clone:C130084C11 product:tumor necrosis factor receptor RESULT 3 Q8C4K3 8844488 ò ò

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SMART; SM00208; TNFR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Tnfrsf14;
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                 Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                     186
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Matches
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STRAIN=CS7BL/6J; TISSUB=Head;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
A Hori F., Indocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M.,
A Katoh H., Kawai J., Kojima Y., Ohno M., Ohsato N., Okazaki Y.,
A Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Sato R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (APR-2002) to the BubL/Genbank/DDBJ databases.
B. Bubli, AKOS1879; Baccos Tote Engledensk/DDBJ databases.
B. GO; GO: OOOS615; C: Cextracellular space; TAS.
B. GO; GO: OOOS615; C: Cextracellular space; TAS.
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ECYBL/GJ; IISSUE=Head;
The FANTOM CONSORtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Head; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramateu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                               SEQUENCE FROM N.A.
STRAIN=CS7BL/60; TISSUE-Head;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CSPBL/64); TISSUE-Head;
STRAIN-CSPBL/64); PubMed-11076861; DOI=10.1101/gr.152600;
Shibata E., Itch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itch M.,
Sumi N., Ishii Y., Nakamura S., Hazawa M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
               Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
VOLE_TaxID=10090;
                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSOTTium;
member 18, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR006210; IEGF.
InterPro; IPR001368; TNFR_C6.
                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Head;
                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
superfamily,
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125
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                                                                                                                                                    65
                                                                                                                                                                                                 53
                                                                                                                                                                                 66 CCSEWDCMCVQPEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGHE
                                                                                                                                                                                                                                                                                                                                                        GHCKPWIDCIQFGFLIVFPGNKIHNAVCVPGSPPABPLGWLIVVLLAVAACVLLLISAQL
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                                                                                                                                                 7 MGAFRALCGLALLCALSLGQ-RPTGGPGCGPGRLLLGTGTDARCCRVHTTRCCRDYPGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 LSLGQRPTGGPGCGPGRLLLGTGTDARCCRV----HTTRCCRDYPGEEC-----
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                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLHIWQLRSQCMWPRETQLLLEVPPSTEDARSCQFPEEERGERSAEEKGRLGDLW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74;
                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor receptor superfamily member 14 precursor.
                                               Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coukos G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 275;
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                                                                                                 Indels
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STRALN-67-PL/6; TISSUE-Thymus;
STRALN-67-PL/6. TISSUE-Thymus;
Benencia F., Conejo-Garcia J.R., Courreges M.C., Coukos
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 275 AA; 30171 MW; C4A7EAD8EFC0521D CRC64;
250 AA; 27814 MW; 6963E94F414C16B4 CRC64;
                                               / Match 53.1%; Score 735.5; DB 2; Local Similarity 57.0%; Pred. No. 1.7e-54; nes 134; Conservative 31; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.6%; Score 202; DB 2; 24.6%; Pred. No. 3.6e-09; ative 32; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:2075303; Thirsf14.

MGD; MGI:2075303; Thirsf14.

GO; GO:0004089; F:transmembrane receptor activ

GO; GO:0004089; F:transmembrane receptor activ

GO; GO:0006915; P:apoptosis; IEA.

GO; GO:0007085; P:immune response; IEA.

GO; GO:0007165; P:immune response; IEA.

InterPro; IPR003063; Fas receptor.

InterPro; IPR001368; TNFR_G6.

Pfam; PF00020; TNFR_G6; 3.

PRINTS; PR001080; TNFR 66; 3.

PRINTS; RN01080; TNFR 66; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 1.
PROSITE; PS50050; TNFR NGFR 2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Potential
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[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                antigen 4-1BB.";
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KESULT 6
TNR9_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 PPGOGVQSQGKFSFGFQCIDCASGTFS-GGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203
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                                     PPGQGVQSQGKFSFGFQCIDCASGTFS-GGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVC 153
                                                                               154 VPGSPPAEPLGWLTVVLLAV----AACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30 INLIGRISAQPSCRQEBFLVGD----ECCPMCNPGYHVKQVCSEHTGTVCAPCPPQTYTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 HANGLSKCLPCGVCDPDMGLLTWQECSSWKDTVCRCI-PGYPCENQDGSHCSTCLQHTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----CSEWD---CMCVQPEFHC----GDPCCTTCRHHPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 VPGSPPAEPLGWLTVVJLAVA----ACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----HTSSVAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=129/SvJ;
Rickert S., Granger S.W., Ko M., Shukla D., Spear P.G., Kronenberg M.,
Ware C.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 LSLGQRPTGGPGGPGRLLLGTGTDARCCRV-----HTTRCCRDYPGEEC-----
                                                                                                              204 ----SSQVVYYVVSILLPLVIVGAGIAGFLICTRRHLHTSSVAKE------LE-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF515707; AAQ08183.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006915; P:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR008063; Fas receptor.
InterPro; IPR008063; Fas receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4A615FB2629E9125 CRC64;
                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Herpes virus entry mediator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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----SSQVVYYVVSILLPLVIVGVGIAGFLICTRRHL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 14.5%; Score 201.5; DB Similarity 23.9%; Pred. No. 4e-09; 64; Conservative 35; Mismatches E
                                                                                                                                                                                                                                                          276 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 VPPSTEDAR -- SCOFPEERGERSAEEK 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 LEPFOQEQGENTIRFPVTEVGFAETEEE 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00020; TNFR_c6; 3.

PRINTS; PR01680; FASRECEPTOR.

SMART; SM00208; TNFR; 4.

PS0051TE; PS00652; TNFR NGFR_1; UNKNOWN_1.

PROSITE; PS50050; TNFR NGFR_2; 3.

SEQUENCE 276 AA; 30\overline{2}77 M\overline{4}7, 4A615FB262
                                                                                                                                             210 PSTEDARSCQFPEEERGERSAEEK 233
                                                                                                                                                                   248 FQEQQENTIRFPVTEVGFAETEEE 271
                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                       Name=Hvem;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    similarity).
    SUBCELIULAR LOCATION: Type I membrane protein.
    TISSUE SPECIFICITY: Expressed on the surface of activated T cells.
    INDUCTION: Optimal by PMA and ionomycin.
    SIMILARITY: Contains 4 TNFR-Cys repeats.

                                            01-FEB-1991 (Rel. 17, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen)
Mame=Tnfref9; Synonyms=Cd137, Cd157, ILA, Ly63;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; J04492; AAA40167.1; -.

R EMBL; U02567; AAA3113.1; -.

R PDB; 1DD01; X-ray; G/H/L/J/K-230-236.

R MG1: MG1:1101059; Thfref2.

R InterPro; IPR001369; TNFR_c6.

R InterPro; IPR001369; TNFR_c6.

R PROSITE; PS00050; TNFR_C6; 1.

R PROSITE; PS00052; TNFR_NGFR_1; 1.

R PROSITE; PS00050; TNFR_NGFR_1; 1.

R PROSITE; PS00050; TNFR_NGFR_1; 1.

R PROSITE; PS50050; TNFR_NGFR_1; 1.

R PROSITE; PS00130; TNFR_NGFR_1; 1.

R PROSITE; PS00130; TNFR_NGFR_1; 1.

R PROSITE; PS0131; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kin K.K., Pickard R.T., Kwon B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Immunol. 150:771-781(1993).
-!- FUNCTION: Receptor for INFSF14/4-1BBL. Possibly active during T cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: Principally an homodimer, but also found as a monomer. Associates with p56-LCK. Interacts with TRAF1, TRAF2 and TRAF3
                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                       MEDIJINE-94179905; PubMed-8133039;
Kwon B.S., Kozak C.A., Kim K.K., Pickard R.T.;
"Genomic organization and chromosomal localization of the T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Inducible T cell antigen 4-1BB. Analysis of expression and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            superfamily member 9.
Extracellular (Potential).
Potential.
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                                                                                                                                                                                                                                                         MEDLINE-89184547; PubMed=2784565;
Kwon B.S., Weisean S.M.;
"cDNA sequences of two inducible T-cell genes.";
Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989)
 256 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION, AND SEQUENCE OF 24-29.
MEDLINE=93139510; Pubmed=7678621;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Immunol. 152:2256-2262(1994).
TNR9_MOUSE STANDARD;
P20334;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last seq
25-OCT-2004 (Rel. 45, Last ann
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T Tmmunol. 150:771-781(1993)
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208
256
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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188
209
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TRANSMEM
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 KDVVCGPPVVSFSPSTTISVTPEGGPGGHSLQVLTLFLALTSALLLAL-----IFITLL 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-94085794; PubMed-8262389; DOI=10.1016/0378-1119(93)90110-O; SChwarz H., Tuckwell J., Lotz M.; A receptor induced by lymphocyte activation (ILA): a new member of the human nerve-growth-factor/tumor-necrosis-factor receptor family."; Gene 134:295-298(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPPSTFSSIGGQPNCNICRV---CAGYFRFKKFCSSTHNAECECIE-GFHCLGPQCTRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 HNAVCVP------GSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECGSEW---DCMCVQPEFHCGDPCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alderson M.R., Smith C.A., Tough T.W., Davis-Smith T., Armitage R.J., Falk B., Roux E., Baker E., Sutherland G.R., Din W.S., Goodwin R.G., "Molecular and biological characterization of human 4-1BB and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O1-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB ligand receptor) (T-cell antigen 4-1BB homolog) (T-cell antigen ILA)
(CD137 antigen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                        N-linked (GlcNAc. . .) (Potential) N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 256;
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-heg 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 RSQCMWPRETQLLLEVPP----STEDARSCQFPEEERG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 FSVLKWIRKKFPHIFKQPFKKTTGAAQEEDACSCRCPQEEEG 249
                                                                                                                                                                                                                                                                                                                                                                                                          93A10D03C60813C4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.2%; Score 197; DB 1;
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TNFR-Cys 1.
TNFR-Cys 2.
TNFR-Cys 3.
TNFR-Cys 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=TNFRSF9; Synonyms=CD137, ILA;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94374434; PubMed=8088337;
                                                                                                                                                                                                                                                                                                                                                                                                             27598 MW;
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93
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [3]
REVISION TO 107
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**XENUERCHAIREY; **PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Rownstein M.J., Usdin T.B., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Basak S.A., McKwan P.J., McKernan R.J., Malek J.A., Gunarathe P.H., N. Richards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hulyk S.W., Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abutting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Raterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND VARIANTS THR-56; ASN-115 AND ASP-176. Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W., Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A., "NIERS-SNPS, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)."; Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
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                                                                                           msbulnk=95347766; PubMed=7622190; DOI=10.1016/0165-2478(94)00227-I;
Zhou Z., Kim S., Hurtado J., Lee Z.H., Kim K.K., Pollok K.E.,
Kwon B.S.;
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MEDLINE=98078711; PubMed=9418902;

Arch R.H., Thompson C.B.;

Arch R.H., Thompson C.B.;

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Goldstein M.D., Bangia N., DeBenedette M.A., Mak T.W., Choi Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA sequences.";
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MEDLINE=21662677; PubMed=11804328;
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PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
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MEDLINE=98270914; PubMed=9607925;
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J. Exp. Med. 187:1849-1862(1998)
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NCBI_TaxID=9685;
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MIM; 602250; -...

R GO; GO: 0005887; C: integral to plasma membrane; TAS.

R GO; GO: 0005887; C: integral to plasma membrane; TAS.

R GO; GO: 0006817; P: receptor activity; TAS.

R GO; GO: 00068285; P: negative regulation of cell proliferation; TAS.

R GO; GO: 0008285; P: negative regulation of cell proliferation; TAS.

R INTERPO; IRREQUISE; TAPR C6; 2.

R PROSITE; PS00652; TAPR NGFR 1; 1.

R PROSITE; PS00652; TAFR NGFR 2; 1.

R PROSITE; PS00650; TAFR NGFR 2; 1.

R Direct protein sequencing; Glycoprotein; Polymorphism; Receptor;

R Repeat; Signal; Transmembrane.
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F3A563FE5EF00460 CRC64;
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Extracellular (Potential)
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EMBL; L12964; AAA62478.2; -.
EMBL; AA438976; AAR05440.1; -.
EMBL; AL009183; CAB57388.1; -.
EMBL; BC006196; AAH06196.1; -.
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Genew; HGNC:11924; TNFRSF9.
H-InvDB; HIX000096; -.
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                                                                                                                                                                                                                                                                                                                                                            145 GNKTHNAVCVPG-----SPPA---EPLGWLTVV--LLAVAACVLLLTSAQLGLH 188
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                                                                                                                34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPG-----EECCS----EWDCMCVQPEFHCGDP 84
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                                                                                                                                                                         48 CPPNSFSSAGG--QRTCDI----CRQCKGVFRTRKECSSTSNAECDC---TPGFHCLGA
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Akashi H., Takeuchi Y., Hosie M.J., Willett B.J.;
"Use of CD134 as a primary receptor by the feline immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O5-509.

O5-JUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CD134 homologue.
CD134 homologue.
CD134 homologue.
CD134 homologue.
CAPLIS silvastria catus (Cat.)
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
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   Length 255;
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                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 AA; 28731 MW; 36A40BAD261140D1 CRC64;
14.1%; Score 195.5; DB 1; 28.8%; Pred. No. 1.2e-08; iive 21; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB128982; BAD11363.1; -. GO, GO:0004872; F:receptor activity; IEA. InterPro; IFR001368; TNFR_c6. Fam: PF00020; TNFR c6; 2. SMART; SM00208; TNFR; 3. PROSITE; PS000652; TNFR NGFR_1; 2. PROSITE; PS50060; TNFR NGFR_1; 2. SEQUENCE: PS50050; TNFR NGFR_1; 2. SEQUENCE: 270 AA; 28731 MW; 36A40BAD2611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65; Conservative
                                                                66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 0:0-0(2004).
                      Best Local Similarity
Matches 66; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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177 PYRPPTA----
  HSSP; Q92956; 1JMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 CQFPE 222
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                                                                                                                                                   Signal.
NON TER
SIGNAL
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Best Local 9
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                                                                                                                                                                                                                 CHAIN
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Q9DDD2
                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 DCMCVQPEFHCGDPCCTTC-RHHPCPPGQGVQSQGKFSFGFQCIDCASGTFSGGH--EGH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 PCICLL-GFHCSSGTCVTCVPHATCKPGQWAKIKGNLTHDTVCESCPEGSFSTSHSWSSV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 CKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVL----LAVAACVLLLTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 QLGLHIWQLRSQCMWPRETQLLLEVPPS-----TEDARSCQFPEEER---GERSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 CGPGTRRMSQSTCTDPQCAECGNREYQDRYTREAQCKRQPYCDPNKNLRVTKPESKTKQS
                                                                                                                                                Paralichthys olivaceus (Japanese flounder).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryccolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 290;
                                                                                                                                                                                                                                                                                                                                                                                    Park C., Hirono I., Aoki T.;
Park C., Hirono I., Aoki T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB08175; Fireceptor activity; IBA.
InterPro; IPR06209; EGF like.
InterPro; IPR001368; INFR_CS.
SMART; SM00208; TNFR; 2.
PROSITE; PS00186; EGF 2; UNKNOWN I.
PROSITE; PS00186; EGF 2; UNKNOWN I.
SEQUENCE 290 AA; 32396 MW; B6FCF9E35305DFAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB003911; BAA20059.1; -.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Park C., Hirono I., Aoki T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.2%; Score 182.5; DB 2; Best Local Similarity 25.8%; Pred. No. 1.7e-07; Matches 63; Conservative 24; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 CGPG--RLLLGTGTDARCCRVHTTRCCRDYPGEECC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 AA
    290 AA
                                              Created)
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    PRT;
                                          (TrEMBLrel. 27, C
(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
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    PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                           NCBI_TaxID=8255;
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Q76LB4;
Q76LB4;
05-JUL-2004 (
05-JUL-2004 (
05-JUL-2004 (
                                                                                                                                 Name=CD40
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61 YPG--EECCSEWDCM-CVQ-----PEFHCGDPCCTTCRHHPCPPGQGVQSQGKFSFG 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110 FOCIDCASGTFSGGHEGHCKPWTDCTOFGFLTVFPGNKTHNAVC-------VPGS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158 PPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPSTEDARS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .-----RTSTAWPRTAQ-----GPSTPTLEA 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 ALCGLA-LLCALSLGQRPTGGPGC-----GPGRLLL----GTGTDARCCRVHTTRCCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AALGLALLLLGLLLGAEPR--PDCVGDTYPGGDRCCLECQPGYGMVSRCNRSQDTICHPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 VDCAPCPQGHFSEGNNRACRPWTNCTLAGKRTLQPASSISDAVCEDRSSLATQPWETPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tregaskes C.A.;
Thesis (2001), University of Reading, Reading, UNITED KINGDOM
EMBL; AZ29310); CRC20218.1; -.
HSSP; Q92956; 1JMA.
                                                                                                                                                                                                                                                                                                                                                                                                 Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0016020; C:membrane; IEA.
GO; GO:0016089; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptoclas; IEA.
GO; GO:0006915; P:apoptoclas; IEA.
GO; GO:0006915; P:aignal transduction; IEA.
GO; GO:0007165; P:immune response; IEA.
GO; GO:0007165; P:immune response; IEA.
GO; GO:0007165; P:immune response; IEA.
GO; GO:0007165; P:immune response; IEA.
GO; GO:0007165; P:immune response; IEA.
GO; GO:0007165; P:immune response; IEA.
InterPro; IPR001005; MyPR_Co.
Fram; PF00020; TWRR Co.
SMART; SM00208; TWRR, G.
SMART; SM00208; TWRR, I UNKNOWN 1.
FROSITE; PS00652; TWRR NGFR_1; UNKNOWN 1.
FROSITE; PS00652; TWRR NGFR_1; UNKNOWN 1.
FROSITE; PS00652; TWRR NGFR_1; UNKNOWN 1.
FROSITE; PS00652; TWRR NGFR_1; UNKNOWN 1.
FROSITE; PS00652; TWRR NGFR_1; 4040B7E0DB82454E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 ch 13.1%; Score 182; DB 2; Length 26 Similarity 27.8%; Pred. No. 1.7e-07; 68; Conservative 15; Mismatches 88; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; 3.
; 4040B7E0DB82454E CRC64;
                                                                                                                                                                                                                                                               <1 18 Potential.
19 267 0X40.
267 AA; 28489 MW; A8B4CD3173C9500B CRC64;</pre>
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Last annotation update)
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GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00020; TNFR_c6; 2.
BART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50050; TNFR_NGFR_2; 2.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                              16;
                                                                                                                                                                                                                                                                                                                                                                                                                      135
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                                                                                                                                                                                                                                                                                                                                                  51 CNDTEDSVCTPCENGQYQHSWTKERHCTPHEICEDNAGLIVKRHGNATHNTVCQC-RAGM 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                110 HCSDASCOTCVENEPCKQGFGFVAAMAEARMTSPCEPCAEGTFSNVSSKTEPCHFWTSCE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 QFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTSAQLGLHIWQL--- 192
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MEDLINE=94044750; PubMed=8228223;
Calderhead D.M., Buhlmann J.E., van den Bertwegh A.J., Claassen E.,
Noelle R.J., Fell H.;
"Cloning of mouse Ox40: a T cell activation marker that may mediate T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  structure and chromosomal localization of the mouse homologue of
                                                                                                                                                                                                 ---CMCVQPEF
                                                                                                                                                                                                                                                                                                                                                                                                                   80 HCGDPCCTTC-RHHPCPPGQG-VQSQGKFSFGFQCIDCASGTFS--GGHEGHCKPWTDCT
                                                                                                                                                           16 LALLCALSLGQRPTGGPGCG-PGRLLLGTGTDARCCR----VHTTRCC-RDYPGEECCSE
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   precursor (0X40L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193 ------RSQCMWPRETQLLLEVPPSTEDARSCOFPEEER---GERSAEEKGR 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 DLRRRGPKQAEAEAPREL------VTQQPEEVDFPVQETLLGGQPVAQEDGK 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rat OX40 protein.";

Eur. J. Immunol. 25:926-930(1995).

-!- FUNCTION: Receptor for INPSR4/OX40L/GP34.

-!- SUBGNIT: Interacts with TRAF2, TRAF3 and TRAF5 (By similarity).

-!- SUBGRILUTAR LOCATION: Type I membrane protein.

-!- SIMILARITY: Contains 4 INFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                              90; Indels 108;
                           Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=95255413; PubMed=7737295;
Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FFB-1996 (Rel. 33, Created)
01-FFB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 4
                              12.8%; Score 177; DB 2; 24.8%; Pred. No. 4.8e-07; ive 23; Mismatches 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=Tnfrsf4; Synonyms=OX40, Txgp1;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                            ----MD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B cell interactions.";
J. Immunol. 151:5261-5271(1993).
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Query Match
Best Local Similarity 24...
Best Local Similarity 74...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor) (OX40 antigen)
                                                                                                                                                                                                                                                                                            70 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HID BERNESS OF COURT BERNESS SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 -----CTTCRHHP-----CPPGQGVQSQGKFSFGFQCID 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CASGTFSGGHEGHCKPWTDCTQFGFLTVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 CPPGHFSPGNNQACKPWINCTLSGKQTRHPASDSLDAVCEDRS------LLA-- 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 LALTLGVTÄRLINCVKHTYPSGHKCCRECQPGHGMVSRCDHTRDTLC------HPCET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LILGIGIDAR--CCRVHT----TRCCRD-YPG----BECCSEWDCMCVQPEFHCGDPC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=FUB/N; TISSUE=Liver; STRAIN=FUB/N; TISSUE=Liver; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausherg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                             .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           70;
                                                                                   PROSITE; PS00652; TNFR_NGFR_1; 2.
PROSITE; PS50650; TNFR_NGFR_2; 2.
Antigen; Glycoprotein; Receptor; 2.
SIGNAL
SIGNAL
                                                                                                                                      Tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                        7e-07;
----- 70; Indels
                                                                                                                                                    superfamily member 4.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                       06E7BB4156F0D08E CRC64;
                                                                                                                                                                                         Cytoplasmic (Potential). TNFR-Cys 1.
                                                                                                                                                                                                                                (incomplete)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | : : : | | | : | | | 172 --TLLWETQRPTFRPTTVQSTTVWPRTSE--LPSPPT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 ACVLLLTSAQLGLHIWQLRSQCMWPRETQLLLEVPPS 211
                                  response; IMP
                                                                                                                                                                                                                TWFR-Cys 2.

TWFR-Cys 3 (incompl. TWFR-Cys 4.

TWFR-Cys 4.

By similarity.

Nolinked (GlCNAc...
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         MGD; MGI:104512; Tnfrsf4.
GO; GO:0005886; C:plasma membrane;
GO; GO:0006968; P:cellular defense
InterPro; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6; 3.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                          30153 MW;
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124
124
165
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123
139
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HSSP; 092956; 1JMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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63
80
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TRANSMEM
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REPEAT
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REPEAT
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SEQUENCE FROM N.A.
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        Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garrian A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shvychenko Y., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Arrayinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Anders M.A., "Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 CSEWD---CMCVQPEFHC----GDPCCTTCRHHPCPPGQGVQSQGKFSFGFQCIDCASGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.6%; Score 174.5; DB 2; Length 196; Best Local Similarity 27.3%; Pred. No. 5.7e-07; Matches 50; Conservative 28; Mismatches 68; Indels 37;
                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                              receptor activity; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 196 AA; 21555 MW; 2AB3FF8905E260E8 CRC64;
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Last annotation update)
                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                       EMBL: BC02125; AAH22126.1; -...
HSSP; Q92956; 1JVA.

MGD; MG1:267303; JRIEfsf14.

GO; GO:0016620; C:membrane; IEA.

GO; GO:0004888; F:transmembrane receptor activ

GO; GO:0006915; P:immune response; IEA.

GO; GO:0007165; P:immune response; IEA.

GO; GO:0007165; P:immune response; IEA.

FFam; PF00020; TWFR C6; 2.

PRINTS; PRO1660; FASRECEPTOR.

SWART; SM00208; TWFR, 3.

PROSITE; PS50050; TWFR, 2.
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21,
26,
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STRAIN=FVB/N; TISSUE=Liver;
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01-JUN-2002 (TrEMBLrel.
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Name=Tnfrsf9;
Mus musculus (Mouse).
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MEDINE-238825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDINE-238825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Klausberg R.L., Feingold B.A., Magner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B. Buetcw K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusha K., Parmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C., Abrama S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A., Rabey J., Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mithing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Marialez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Abramson M.M., Madan A., Young A.C., Shevchenko A., Schnerch A., Schein J.E., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 RHHPCPPGGGVQSQGKFSFGFQCIDCASGTFSGGH-EGHCKPWTDCTQFGFLTVFPGNKT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 -EKDCRPGQELTKQG-----CKTCSLGTFNDQNGTGVCRPWTNCSLDGRSVLKTGTTE 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 CGPGRL-LLGTGTDARCCRVHTTRCCRDYPGEECCSEW---DCMCVQPEFHCGDPCCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-CHERUS;
Strausberg R.;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
RMBL; BC028507; AA428507.1; -.
RMBL; BC028507; AA428507.1; -.
RMBL; BC028507; AA428507.1; -.
RMBC; MGI-1101059; Thfrsf9.
RGJ; GO:0005615; C:atrearallular space; TAS.
GO; GO:0005615; C:atrearal to membrane; TAS.
RGJ; GO:0005615; C:atrearal to membrane; TAS.
RGJ; GO:0005615; C:atrearal to membrane; TAS.
RINEEPRO; IPR001061; Antihaemostatic.
RINEEPRO; IPR001269; TNFR_C6.
RFGM, PF000209; TNFR_C6.
RFGMRT; SM00209; TNFR_C6; I.
RPROSITE; PS01186; EGF 2; UNKNOWN_1.
RPROSITE; PS006529; TNRF NGFR 1; 1.
SEQUENCE 211 AA; 22452 MW; IEBCA84EA32A8D50 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.3%; Pred. No. 1.3e-06;
tive 22; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 KDVVCGPPVVSFSPSTTISVTPEGGPAFKKTTGAAQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.3%; Score 170.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 25, (TrEMBLrel. 25, (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=CD40;
Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2003 (
01-OCT-2003 (
01-MAR-2004 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7YRL5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7YRL5
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125 EG--HCKPWIDCTQFGFLIVFPGNKTHNAVCVPGSPPAEPLGWLTVVLLAVAACVLLLTS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 CSEWDCMCVQPE-FHCGDPCCTTCRHHP-CPPGQGVQSQGKFSFGFQCIDCASGTFSGGH 124
                                                                                                                                                                                                                                                                                                                                                                                                   34 CGPGRLLLGTGTDARCCRVHTTRCCRDYPGE------BC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
12.3%; Score 170; DB 2; Length 274;
Best Local Similarity 26.1%; Pred. No. 1.9e-06;
Matches 61; Conservative 20; Mismatches 107; Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 AQLGLHIWQLRSQCMWPRETQLLLEVP-----PSTEDARSCQFPEEERGERS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 ACIRKVVKKPENKVMYQDPVEDLEEFPMPPHSIAPVQETLHGCQPVTQEDGKES 266
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
NCBI_TaxID=9615;
                                                                        YEQUENCE FROM N.A.
Yang S., Sim G.-K.;
Submitted (JUL_2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL_2003) to the EMBL/GenBank/DDBJ databases.
HSSP; P25942; 1FLL.
GG; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001368; TNFR.c6.
R Pfam; PF000208; TNFR.c6; 1.
R SMART; SM005208; TNFR; 4.
R PROSITE; PS00652; TNFR, NGFR 1; 1.
R PROSITE; PS00652; TNFR, NGFR 2; 3.
SEQUENCE 274 AA; 30284 MW; 9723789A07FAB6DB CRC64;
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